

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: August 13, 2005, 21:14:42 ; Search time 3738 Seconds

(without alignments) updates/sec
9653.539 Million cell

Title: US-10-018-470A-16

Sequence: 1 atggaatttcattatctt.....gcagcaaacgcccaataa 948

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	18.4	1677	3	AY107408 Zea mays
2	170	17.9	931	3	CNS090CF BX067627 Single re
3	166.8	17.6	890	6	CD789571 B8T660932
4	156.8	16.5	1048	1	AL541792 AL541792
5	156.6	16.5	673	4	B1486916 B8T660932
6	156	16.5	413	8	B2626199 B8T660932
7	155.8	16.4	768	6	CA065919 SCBPA0104
8	155.8	16.4	799	6	CB645833 OSJNB07N
9	155.6	16.4	1071	9	AY408615 Homo sapi
10	155.6	16.4	1073	3	CR594962 full-length
11	155.6	16.4	1095	5	BU508142 AGENCOURT
12	155.6	16.4	1103	3	CR612088 full-length
13	155.6	16.4	1142	3	CR614697 full-length
14	155.6	16.4	1196	3	CR625020 full-length
15	155.6	16.4	1199	3	CR610520 full-length
16	155.6	16.4	1206	3	CR608510 full-length
17	155.6	16.4	1208	3	CR592181 full-length
18	155.6	16.4	1218	3	AF161458 Homo sapi
19	155.6	16.4	1532	3	CR591719 full-length
20	154.4	16.3	1023	5	BX400955 BX400955
21	153.4	16.2	906	7	CO548169 LYEST5061
22	152.2	16.1	947	7	CO5080ND BX020429 Single re
23	151.4	16.0	847	7	CN124718 RH0H_6_B
24	149.4	15.8	897	3	CNS09K89 BX062293 Single re

25	148.8	15.7	657	6	CB620196	CB620196 OS1E05D
26	146.6	15.5	623	4	BM345666	BM345666 rre6e08.y
27	145.4	15.3	712	1	AL722012	AL722012 AL722012
28	145	15.3	906	3	CNS09090	BX070122 Single re
29	144.6	15.3	780	6	CD905963	CD905963 G468.103H
30	144.6	15.3	1062	9	AY408617	AY408617 Mus muscu
31	144.6	15.3	1536	3	AK002793	AK002793 Mus muscu
32	144.2	15.0	705	5	BO579084	BO579084 WHE2965 C
33	142	15.0	1095	4	BM423347	BM423347 AGENCOURT
34	141.8	15.0	648	7	CO532841	CO532841 3530.1.21
35	141.6	14.9	967	7	CO010421	CO010421 EST798756
36	141.4	14.9	918	4	BF263774	BF263774 HV_CBA000
37	140.8	14.9	814	2	BM459766	BM459766 AGENCOURT
38	140.4	14.8	1401	3	CNS0444C	BX826506 Arabidops
39	139.6	14.7	924	3	CNS090CF	BX068923 Single re
40	139.4	14.7	528	1	AV434570	AV434570 AV434570
41	139.4	14.7	954	5	BX441219	BX441219 BX441219
42	138.8	14.6	911	7	CO550654	CO550654 LYEST8914
43	138.6	14.6	492	1	AJ284726	AJ284726 4A3B-AMB
44	138.6	14.6	911	5	BU854863	BU854863 AGENCOURT
45	138	14.6	643	2	BF014265	BF014265 rolph01.y

ALIGNMENTS

RESULT 1
LOCUS AY107408 1677 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PC0142888 mRNA sequence.
ACCESSION AY107408
VERSION AY107408.1 GI:21210486
KEYWORDS
SOURCE
ORGANISM

Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Halney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.

TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes

JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1677)

TITLE Direct Submission
AUTHORS Coe, E.H.
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSU, maize-map.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES
source Location/Qualifiers

1..1677
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Query Match 18.4%; Score 174; DB 3; Length 1677;

Best Local Similarity 52.4%; Pred. No. 1.9e-40;
Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;

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Qy 60 CGTATCCCGCAGAGAGGCTGCAAGTGGGAGGCTGCGGCTTCATCGGCTT 119
Db 337 CATAGTCCGAGAGAGAGGCTTACGTTGTGAGAGATTCGGAGATTCACAGACCT 396
Qy 120 GACGGCGGTTGATATTTGATTCCTTATGACCGCGCTTACCGGCTTACGCT 179
Db 397 CGGCTCCGGTTCCACTCTGATCCCGCGCTGACCGTATTCCTTACGCTGCT 456
Qy 180 GAAAGAAATCCCTTGAAGTACCGACCGAGGCTGATGACGCGCGATTAATGCAAT 239
Db 457 CAAGAGAGAGAGAGAGAGGCTTACCGACCGAGAGAGAGAGAGAGAGAGAGAGAG 516
Qy 240 GACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299
Db 517 ACAAGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 576
Qy 300 GAGCACTACATTAATGCAATTAACCGAGTTCGCCAAGAGAGAGAGAGAGAGAG 359
Db 577 GAGAGATCAATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
Qy 360 GCGATGAGAGTTCGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 637 GAGATTAACCTTAAGTAAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
Qy 420 CGCCCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
Db 697 TGCCATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756
Qy 480 TTTGGTTCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
Db 757 CATTAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816
Qy 540 AAAACGCGCCGCTATTCGCAATTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 599
Db 817 AAAACGCGCTCAATCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
Qy 600 TGGTACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
Db 855 -----AGCGCCCAATCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
Qy 660 GTCCAAATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Db 904 ATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 963
Qy 720 CTTGTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
Db 964 TGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1023
Qy 780 AGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
Db 1024 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
Qy 840 TCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
Db 1084 TCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1129

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RESULT 2
CNS09OCF 931 bp mRNA linear HTC 08-JAN-2003
DEFINITION Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 5-PRIME end of clone
FK0A051BF03 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
ACCESSION BX067627
VERSION BX067627.1 GI:27640908
KEYWORDS HTC
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 931)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
location/Qualifiers

FEATURES
source
1..931
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0A051BF03"
/plasmid="pME18S-FL"
/note="end : 5-PRIME"

ORIGIN

Query Match 17.9%; Score 170; DB 3; Length 931;
Best Local Similarity 54.3%; Pred. No. 2.6e-39;
Matches 364; Conservative 0; Mismatches 305; Indels 1; Gaps 1;

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Qy 65 TCCCCAGCAGAGAGTCCAGCTGTCGAAAGAGCTGCGGCTTCATCGCGCTGACGG 124
Db 256 TGCCCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 315
Qy 125 CCGGTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTT 184
Db 316 CCGGCTGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 375
Qy 185 AATCCCTTGAAGAGTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
Db 376 AATTCGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
Qy 245 TTGACGAGATCATATTTTCCAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304
Db 436 TCGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
Qy 305 ACTACATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 496 ACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
Qy 365 TGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 556 TGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
Qy 425 TCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
Db 616 TCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
Qy 485 TTGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
Db 676 AGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
Qy 545 GCGCGCGATTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
Db 735 GGGCGCGAGATCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794
Qy 605 AGCGTGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664
Db 795 AGCAGAGTGGCGGATCTTGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
Qy 665 ATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 724
Db 855 ATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
Qy 725 TTGCGGAGAG 734
Db 915 TGCGGAGATC 924

```

RESULT 3

CD789571 890 bp mRNA linear EST 01-JUN-2004
 LOCUS CD789571 RAB Rhinipcephalus appendiculatus cDNA clone RABAJ94 5'
 DEFINITION end, mRNA sequence.
 ACCESSION CD789571
 VERSION CD789571.1 GI:49545245
 SOURCE EST
 ORGANISM Rhinipcephalus appendiculatus
 Rhinipcephalus appendiculatus
 Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhinipcephalus.
 1 (bases 1 to 890)
 Nene, V., Lee, Y., Skilton, R., Mwaura, S., Quackenbush, J., Gardner, M.
 and Bishop, R.
 TITLE An index of genes transcribed in the salivary glands of
 Rhinipcephalus appendiculatus
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: EST660931
 Contact: Vishwanath Nene
 Parasite Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-610-5968
 Fax: 301-838-0208
 Email: nene@igr.org
 Seq primer: M13 reverse.
 Location/Qualifiers
 1..890
 /organism="Rhinipcephalus appendiculatus"
 /mol_type="mRNA"
 /strain="Muguga"
 /db_xref="taxon:34631"
 /clone="RABAJ94"
 /dev_stage="Adult"
 /lab_host="E. coli strain DH10B-Tona"
 /clone_lib="RAB"
 /note="Organ: Salivary gland; Vector: pCMVSPORT6.0.cdbd;
 Salivary glands were dissected on day four after
 initiation of feeding. Total RNA was prepared using acid
 guanidium thiocyanate-phenol-chloroform extraction. The
 cDNA library was custom prepared by Invitrogen
 Corporation. Briefly, first strand cDNA was primed using
 oligo(dT) containing a NotI site. Size fractionated double
 stranded cDNA was ligated to EcoRV-NotI cleaved vector and
 electroporated into E.coli. Library RAB was made from
 ticks infected with Theileria parva."

ORIGIN
 Query Match 17.6%; Score 166.8; DB 6; Length 890;
 Best Local Similarity 53.0%; Pred. No. 2.3e-38;
 Matches 357; Conservative 0; Mismatches 317; Indels 0; Gaps 0;

56 TTGTGCTATCCCCGAGCAAGTCCAGTTGTGCAAGGCTCGGCGTTCCATCGCG 115
 192 TTATGTTGTACTCAACAAGAGCAATGAGTGTGTCAGAGAGTGAAGTTCGCGAA 251
 116 CCTGACGCGCGTGTGATATTTGATTCCTTTATCGACGCGTTCGCTACCGCATT 175
 252 TACTGAGCGCGTGTGATCTGCTCTCCGTATACCGTGTAGCGTATGTGCAAT 311
 176 CGCTGAAGAAATTCCTTTAGACGTACCGACCGAGCTGTCATACGCGCGATATACGC 235
 312 CACTCAAAAGAAATAGCATCGACATCCCGACAGCATCTCCATTAAGCTAGACAAAGTGA 371
 236 AATTGACTGTGACCGCATCATCTATTTCCAGTAACGATCCCAAACTGCGCTATAGC 295
 372 CGCTCAACATCGACGCGGTCTTCTTACCTGAAGTGTGACCAATATCGGCGAGCTAGC 431
 296 GTTCGAGCAACTATATGCAATTAACCGAGCTTCCCAAGACGCTGCGTTCCGTTA 355
 432 GCGTCAGAGACCCCGAATTCGCATACGAGCTGCGACAGACACGATGCGCTCGAGC 491
 356 TCGGCGGTATGAGTTGACAAACGTTGAGAGACGCGACGAATCAACATGACCGTGC 415

DB 492 TCGCAAGATAGCGCTGCACAGCGTCTTCAAGAGCGCGAGATCTCTCAACATTCGCATTG 551
 416 TCTCCGCCCTTGAATGAAGACCCCGCGGCTTGGGGGTGAAGATCTCTCGTACGAATCA 475
 DB 552 TGAATGCCATCAACAAGCGAGCGGTGTGTGGGATCTGTGCTGCGTACGAGATCC 611
 476 AGAATTTGGTTCGCGCGCAAGAAATCTTCCCGCAATGCAGACCAAAATTAACCCGCAAC 535
 DB 612 GCGACATACGCTTCTTCAACAGCGGCTTCCAGCAAGCATGTCAATGCAATCGAAGCCGAGC 671
 672 GGAAGAAAGAGGCGGCACTTCTGAGTCTGAAGAAATTAAGAAAGACATATCAACGTAG 731
 536 GCGAAAAACGCGCCCGTATTCGCGAATCGAAGCGGTAAATGCAACAAATCAACCTTG 595
 DB 672 GGAAGAAAGAGGCGGCACTTCTGAGTCTGAAGAAATTAAGAAAGACATATCAACGTAG 731
 596 CCAAGTGTACGCTGTAAGCCGAATTCGAATTCGAAGGCGGAGGCTAGCGTGGCTCA 655
 DB 732 CCGAGGGGCAAGCGCGCTGCGGCAATCTGAGCTTGGAAAGCCGAAGATGAGCTAATTA 791
 656 ATGCGTCAATGCGGAGAAATTCGCGCATCAACCGGCGCAAGGCGGAGCGGAATCCC 715
 DB 792 ACAAGCGCGATGCGGAGCCCAACGCGCAGCTTCCCAAGCTGAGGCGCAAGGCGCAAGGCC 851
 716 TCGCGCTTGTGCTG 729
 DB 852 TTAGCGAATAGCC 865

RESULT 4
 AL541792 1048 bp mRNA linear EST 24-MAR-2004
 LOCUS AL541792 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE007YE18
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION AL541792
 VERSION AL541792.3 GI:45717369
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euteleostomi; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1048)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:30546303.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5178.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DE007HC09P16c=5178.r.
 Location/Qualifiers
 1..1048
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 /mol_type="mRNA"
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 /clone="CS0DE007YE18"
 /issue="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with NotI and EcoRV sites of the
 pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
 Query Match 16.5%; Score 156.8; DB 1; Length 1048;

Best Local Similarity 50.6%; Pred. No. 2.4e-35;
Matches 432; Conservative 1; Mismatches 388; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGAGAGAGTCCAGCTTTCGAAAGGCTCGGGGCTTTCATGCGCCCGCA 121
Db 2 TCGTCCGCGACAGAGAGCTCGGGGCGAGCGAATGGCGAATTCACCGGATCCTGG 61
QY 122 CGGCGCGTTTGAATTTGATTCCTTTATCGACCGCGTGCCTTACCGCATTCGCTGA 181
Db 62 AGCCGTGGTTGAACATCCTCATCCCTGTGTTAGACCGATCCGATATGTGACAGTCTCA 121
QY 182 AAGAAATCCCTTGAAGCTTACCGCCAGCGTTCGATACCGCGGATTAATGCAATTGA 241
Db 122 AGGAAATGTGATCAACGTGCTGAGCAGCGGCTGTGATCTCGACAAATGTAATCTGCG 181
QY 242 CTGTGTAAGGATCATCTATTTCCAGATACCGAATCCCAACTGCCCTCATAGGTTTGA 301
Db 182 AAATCGATGAGAGCTCTTAACTCGCGCATATGACCTTTACAGGCAAGCTACGGTGG 241
QY 302 GCAACTACATTATGCGCAATTAACCGCTTTCGCAAGACGCGTTCGCTTATCGGCG 361
Db 242 AGGACCCGAGATATCCCTCACCGAGCTTACGTAACCAACATGATCAAGCTCGCA 301
QY 362 GTATGAGATTGAGCAAAACGTTTGAAGACGCAAGAAATCAACATACGCTGCTTCG 421
Db 302 AACTCTCTGTGACAAAGTCTTCGCGGAAAGGAGTCCCTGAATGCGACATTTGGATG 361
QY 422 CCCTCGATGAAAGCGCGCGGCTTGGGGTGTGAAAGTCTCCCTTACCAATCAAGATT 481
Db 362 CCATTCATCAACAGCTGCTGATGCTGGGGTATCCGCTGCTCTGTTATGATCAAGGTA 421
QY 482 TGGTTCCGCGCAAGAAATCCTTGGCGGATGACGACAAATTAACCGCGCAAGCGCAA 541
Db 422 TCATGTGTCACCCCGGCTGAAAGATCTATGACATGACAGTGAAGGCAAGCGCGGA 481
QY 542 AACGCGCCGATTTGCGCAATCCGAAGCCGTAATGAAACAAATCAACCTTGCGAGTG 601
Db 482 AACGCGCCAGATTCTAGATCTGA-----GG 508
QY 602 GTACGCGTGAAGCCGAATTCACCAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCT 661
Db 509 GAAACCCGAGATCGGCGCATATGTGCGAAGGGAAGAAACAGGCCCAAGATCCTGGCCT 568
QY 662 CCAATGCGGAGAAATCGCCCGCATCAACCGCGCAAGCGGAAGCGGATCCCTGCGCC 721
Db 569 CCGAAGCGAAGAGGCTGAACGATTAATCAAGGCGAGGAGAGGCCAGTCAAGTTCTGG 628
QY 722 TTGTTGCGGAAGCCATGCGCAAGCCATCGTCAATTTGCGCGCCCTTCAAAACCAAG 781
Db 629 CGAAGCGCAAGGCTTAAGCTGAAGTATTCGAATCTGGCTGCAAGCTTGAACAACATA 688
QY 782 GCGGGGCGGATGCGGTCAATCTGAAGATTGCGGAACATACGTAAGCCGCTTCAACAATC 841
Db 689 ATGAGATGACAGAGCTTCACTGACTGTGGCGGACGATATGTGACCGCGTTTCCAAAC 748
QY 842 TTGCGAAGAAAGCAATACGCTGAATTATGCCCGCAATGTTGCGCAATCGGAGCGCTGA 901
Db 749 TGGCGCAAGACTCCAAACATATCTAATGCTCCCAACCTTGGGATGTCAACGACATGG 808
QY 902 TTTCTGCGCGCATG 915
Db 809 TGGCTCAGGCGCATG 822

RESULT 5
BI486916 673 bp mRNA linear EST 28-AUG-2001
LOCUS RE70403.5prime RE Drosophila melanogaster normalized Embryo pfic-1
DEFINITION Drosophila melanogaster cDNA clone RE70403.5 similar to CG2970:
Fban0002970 GO:[] Located on: 2R 60A12-60A13; 05/17/2001, mRNA
sequence.
ACCESSION BI486916
VERSION BI486916.1 GI:15326585

KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 673)
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B.,
Carlson,J., Champagne,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,
George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
Miera,S., Mangall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
Rubin,G.M.
TITLE BDGP/HMT RE Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST/est@fruitfly.berkeley.edu>
hit genomic: AB003462: arm:2R [18701964,19002505]
estimated-cyto:60A1-60B4: 05/17/2001
Plate: RE.704 row: A column: 3
High quality sequence stop: 623.
Location/Qualifiers
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE70403"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DHS-alpha Tona"
/clone_id="RE Drosophila melanogaster normalized Embryo
pfic-1"
/note="Organ: embryo; Vector: pfic1; Site.1: XhoI; Site.2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

ORIGIN
Query Match 16.5%; Score 156.6; DB 4; Length 673;
Best Local Similarity 52.6%; Pred. No. 2.4e-35;
Matches 339; Conservative 0; Mismatches 305; Indels 0; Gaps 0;

QY 29 CGTGGCGGTTTGGCTTCAATCTTTGTGTCATCCCCCAGAGAACTCCAGTTG 88
Db 26 CGGTGCGCGGAGCTCACTCCAAATCCGATCGTTCCTCGTTTCCAGGCTGGGTGG 85
QY 89 TCGAAGGCTCGGGCGTTTCATGCGGCCCGTGAAGCGCGGTTGAATATTTGATTCCT 148
Db 86 TGGAGCGCATGAGGGCGCTTTCACAGATTTTGAACCCCGGACTAACAATACTAGTCCGG 145
QY 149 TTATGACCGCGGTGCGCTTACCGCATTCGCTGAAGAAATCCCTTGAAGTACCGAGCC 208
Db 146 TGGCGGACAAATTAATATAGCTCCAGAGCTGGAAGAAATTTGCATGATGTGCCAAAC 205
QY 89 TCGAAGGCTCGGGCGTTTCATGCGGCCCGTGAAGCGCGGTTGAATATTTGATTCCT 148
Db 86 TGGAGCGCATGAGGGCGCTTTCACAGATTTTGAACCCCGGACTAACAATACTAGTCCGG 145
QY 149 TTATGACCGCGGTGCGCTTACCGCATTCGCTGAAGAAATCCCTTGAAGTACCGAGCC 208
Db 146 TGGCGGACAAATTAATATAGCTCCAGAGCTGGAAGAAATTTGCATGATGTGCCAAAC 205
QY 209 AGGTCTGATCAACGCGGATTAATACGAATTGACTGTGAAGGATCATTAATTTCAAG 268
Db 206 AGAGCGCTATTAACCTCGGACAAAGCTGAGACCTGAGCATGACGCGGCTCTCATTTGGCA 265
QY 269 TAACCGATCCCAACTGCGCTCATAGGTTGAGCAACTATATGGAATTAACCAAGC 328
Db 266 TCATTGATTCGTAACAAAGCTCTGTAACGCGGTGAGATTCGGAATTCGCAATACAAAC 325
QY 329 TTGCGCAAGACGCGCTGTTCCGTTATCGGGCGTATGAGATTTGACAAACGTTGAAG 388
Db 326 TGGCGGACGAGCATATAGATCGAGCTGGGCAAGATGTCTCATGACAAAGTCTTCCACG 385
QY 389 AACCGGACGAATTAACAGTACCGTCTTCGCGCTCGATGAAGCGCGGGGCTTGGG 448
Db 386 AAAGGAGTCCCTCAAGGTGAGATGCTGATCAACAAAGGCCAGCGAGGCGTGGG 445

QY 449 GTGTGAAGTCTCTGTTAGCAATGAAATTGGTTCGCCGCGAAGAAATCTTCCG 508
 Db 446 GCATCGCTGTCTGATGATGAGATCCGTGATATTCAGCTGCCCAAGGGTTCCAGAG 505
 QY 509 CAATGACGACCAATTTACCGCCGAAAGCGGAAAGCGGCGTATTTGCGCAATCCGAG 568
 Db 506 CGATGCAATGCAATGAGAGCGCGGCGGAAAGCGGCGTATTTCTCGAATCGAGG 565
 QY 569 GCCGTAAATGCAATCAACTTTCAGTGTCTGACGTTGAGAGCCGAAATTCACAAT 628
 Db 566 GTGTTCGAGAGCGCAAAATCAATACCGAGGCGAAGCGAAGTCTAGATTGAGCT 625
 QY 629 CGAAGCGAGGCTCAGGCTGCGTCAATGCTTCATGCGAG 672
 Db 626 NCGAGGCGGAGCGGAGGACATCAATTAAGCGCAGGAGAG 669
 RESULT 6 413 bp DNA linear GSS 17-JAN-2003
 LOCUS B2626199
 DEFINITION B2626199.1 MGS-Sbicolorf (DH5a methyl filtered) Sorghum bicolor genomic clone 1h44c01 5', genomic survey sequence.
 ACCESSION B2626199
 VERSION B2626199.1 GI:27778284
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 Kaczenburger, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Zuteven, J., Palmer, L., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
 CONTACT: W. Richard McCombie
 Lila Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: 1h44 row: c column: 01
 Seg primer: -21M13univFwd
 Class: shotgun
 High quality sequence stop: 413.
 Location/Qualifiers
 1..413
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /db_xref="taxon:4558"
 /clone="1h44c01"
 /lab_host="DH5a"
 /note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed into DH5a."
 ORIGIN
 Query Match 16.5%; Score 156; DB 8; Length 413;
 Best local Similarity 63.9%; Pred. No. 3.2e-35;
 Matches 271; Conservative 0; Mismatches 120; Indels 33; Gaps 1;
 QY 473 TCAGAGATTGGTTCCCGCGCAAGAAATCTTGGCGCAATGACGCGCAATTAACGCCG 532
 Db 11 TCAGAGACTGACCGCGCAAGAAATCTTGCACGCGCAATGACGCGCAATCAACGCCG 70

QY 533 AAGCGAAAAAGCGCGCGTATTTGCGCAATCCGAAGCGCGTAAATCGAACCAATCAAC 592
 Db 71 AGCGGAAAAAGCGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 130
 QY 593 TTGCGAGTGTCTGACGCGTGAAGCGCGCAATTCGAATCGAAGCGCGTATTTGCGCG 652
 Db 131 TCAGCAACGCGTGAAGCGCGCAATTCGAATCGAAGCGCGTATTTGCGCGTATTTGCGCG 188
 QY 653 TCAGTGTCTGCAATGCGCGCAAGAAATTCGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 712
 Db 189 -----CATCAACGTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 217
 QY 713 CCTGCGCGCTTTGTTGCGCGCAATGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 772
 Db 218 CCATCTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 277
 QY 773 AAACCGAAGCGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 832
 Db 278 AGCAGCGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 337
 QY 833 TCAGCAATCTTGGCGCAAGAAATTCGAATCGAAGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 892
 Db 338 TCAGCAATCTTGGCGCAAGAAATTCGAATCGAAGCGCGTATTTGCGCGTATTTGCGCGTATTTGCGCG 397
 QY 893 GCAG 896
 Db 398 GCGG 401

RESULT 7 768 bp mRNA linear EST 23-SEP-2003
 LOCUS CA065919
 DEFINITION SGBFAD1049A04.g AD1 Saccharum officinarum cDNA clone SGBFAD1049A04 5', mRNA sequence.
 ACCESSION CA065919
 VERSION CA065919.1 GI:34917443
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
 1 (bases 1 to 768)
 Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made STUCST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
 Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: paruda@unicamp.br
 Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
 Plate: 049 row: A column: 04
 Seg primer: T7 Promoter Primer.
 Location/Qualifiers
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 /organism="Saccharum officinarum"
 /mol_type="mRNA"
 /db_xref="taxon:4547"
 /clone="SGBFAD1049A04"
 /lab_host="DH10B"
 /clone="AD1"
 /note="Organ: seedlings inoculated with Gluconacetobacter diazotrophicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from seedlings inoculated with Gluconacetobacter diazotrophicans. cDNA was prepared from polyA+ mRNA using


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RESULT 9
AY408615      1071 bp      DNA      linear      GSS 15-DEC-2003
LOCUS
DEFINITION    Homo sapiens STOML2 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION     AY408615
VERSION       AY408615.1 GI:39764586
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1071)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL       Science 302 (5652), 1960-1963 (2003)
PUBMED        14671302
REFERENCE     2 (bases 1 to 1071)
AUTHORS       Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source        1..1071
               location/Qualifiers
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
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               /gene="STOML2"
               /locus_tag="HCM3283"
ORIGIN
Query Match      16.4%; Score 155.6; DB 9; Length 1071;
Best Local Similarity 50.6%; Pred. No. 5.5e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
QY      62 TCATCCCCCAGAGGAAGTCAAGTGTGAAAGGTCGAGCGCTTCATCGCGCTCA 121
DB      119 TCGTCCGAGAGGAGGCGCTGGGTGTGAGAGCAATGGGCGGATTCACCGGATCTGG 178
QY      122 CGGCGCGTTGAAATTTGATTCCTTATCGACCGCGTCCGCTTACCGCATTCGCTGA 181
DB      179 ACCCTGGTTGAACATCCCTCATCCCTGTGTAGACCGGATCGATATGTGACAGATCTCA 238
QY      182 AAGAAATCCCTTGAAGAGTACCAGCAGAGTGTGATCAGCGCGCATTAATGCAATTGA 241
DB      239 AGGAATTTGTATCAACGTCGCTGAGACAGTCCGCTGTGATCTCGCAATGTAACTCTCG 298
QY      242 CTGTGAGCGGACATCTATTTCCAAAGTAAACGATCCCAACCGCTCATACGTTTCA 301
DB      299 AATATGATGAGAGCTTTTACTCGCGATCATGGACCTTTCAAGGCAAGCTACGAGTGTGG 358
QY      302 GCAACTACATTAATGCAATTAACCAAGCTTGCCTCAAGCAGCGCTGCTCCGTTATCGAGGC 361
DB      359 AGGACCCCTGAGTATGCGCTCACCCAGCTAGCTCAAAACAACATGATCAGAGCTCGGCA 418
QY      362 GTATGAGTTGCAAAAGCTTTGAAGAACGCAAGCAAAATCAACAGTACCGTGTCTCGG 421
DB      419 AACTCTCTCTGCAAAAGCTTTCGGGAAAGGAGTCCCTGATGTCAGAGATGTGTGATG 478
QY      422 CCTGATTAAGCGCGCGCGGCGCTTGGGAGTGTGAAGTCCCTGTTAAGAAATCAAGATTT 481
DB      479 CCAATCAACAGGTGCTGACTGCTGGGGATTCGCGTCTCCGTTATGAGATCAAGATTA 538

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QY      482 TGGTTCGCGCAGAGAAATCTTCGCGCATGCAAGCAGCAAAATTAACGCCAGACGCGAA 541
DB      539 TCATATGTCACACCCCGGATGAAGATCTATGACATGACAGTGGAGCAGAGCGGCGGA 598
QY      542 AACGCGCCGATTTGCGCGAATCCGAAGGCCGTAAATGAAACAATCAACTTGGCAATG 601
DB      599 AACGGCCACAGTTCTAGATCTGA-----CG 625
QY      602 CTCAGCTGAAGCCGAAATTCACAATCCGAAGCGAGGCTCAAGCTCGCGCATATGGGT 661
DB      626 GAGCCGGAAGATCGCCATCAATGTGGCAAGAGGAAACAGGCCCAAGATCTGGGCT 685
QY      662 CCAATGCCAGAAATATCCCGCATCAACCGCGCAAGCGCAAGCGGAATCCCTCGCGC 721
DB      666 CCGAGCGCAAAAGGCTGAACAGATTAATCAAGCAGCAGAGAGGCCAGTGAATTCGG 745
QY      722 TTGTTCCGGAAGCCAAATCCGAAGCCATCCGTAATTTCCGCGCGCTTCAAAACCAAG 781
DB      746 CGAAGGCCAAGGCTTAAGCTGAAGCTATTCGAATCTGGCTGACAGCTCTGACACAACATA 805
QY      782 GCGGCGCGGATGCGGTCAATCTGAAGATTTGGGAAACATATAGTACCGCGTTCAACATC 841
DB      806 ATGAGATGACAGCAGCTTCACTGACTGTGGCGGACAGATATGTGACGCGTTTCCAAC 865
QY      842 TTGCAAGAAAGCAATACGCTGATTATGCCCGCAATGTTGCCGACATCGGACGCTGA 901
DB      866 TGGCCAAAGACTTCAACACTATCTTACTGCTCTCCAAACCTGGCATGTACACCAAGATG 925
QY      902 TTTCTGCGCGCATG 915
DB      926 TGGCTCAGGCGCATG 939
RESULT 10
CR594962      1073 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS
DEFINITION    CR594962      1073 bp      mRNA      linear      HTC 21-JUL-2004
               (human).
               full-length cDNA clone CSDB007YE18 of Placenta of Homo sapiens
               (human).
ACCESSION     CR594962
VERSION       CR594962.1 GI:50475769
KEYWORDS      HTC; CNSLT cDNA.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1073)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@life.techn.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1073)
REFERENCE     Direct Submission
AUTHORS       Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE         BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL       - Web : www.genoscope.cns.fr)
COMMENT       1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
               into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
               was normalized. Library was constructed by Life Technologies, a
               division of Invitrogen.
               location/Qualifiers
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Query Match 16.4%; Score 155.6; DB 3; Length 1073;
Best Local Similarity 50.6%; Pred. No. 5.5e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGCAGAAATCCACGTTGTCGAAAGGCTGGGCGTTTCCATGCGCCCTGA 121
DB 2 TCGTCCCGCAGCAGAGGCTGGGCGTTGTCGAAAGGCTGGGCGTTTCCATGCGCCCTGA 61
QY 122 CGGCGCGTTGAATTTTGAATTCCTTATCGAACCGGCTGCCATCCGCGCATTCGCTGA 181
DB 62 AGCGTGGTTTGAACATCTCTCATCTGTTAGACCGGATCGATATGTCAGAGCTCTCA 121
QY 182 AAGAAATCCTTTAGACGTCACCGACGAGTCTGTCATCAGCGCGATTAATACGAATTGA 241
DB 122 AGGAAATGTGATCAACGTCGCTGAGCGGCTGTGACTCTGCAATGAACTCTGCG 181
QY 242 CTGTTGAGCGCATCTATTTTCCAGTAAGTACCGATCCAACTGCGCTCATACGTTTGA 301
DB 182 AAATCGATGAGTCTTTTACCTGCGCATATGGAACCTTACAGGCAAGCTACGCTGTG 241
QY 302 GCAACTACATTAATGCAATTAACCGCTTGGCCAAAGCGCTGCTTACGTTACGCGC 361
DB 242 AGGACCTGAGTATGCGTCAACCGTACGCTACATCAACATGATGATGAGCTCGCA 301
QY 362 GTATGAGTTGAGCAAAACGTTTGAAGACGCAAGAAATCAACGATACGCTGCTCCG 421
DB 302 AACTCTCTGTGACAAAGTCTTCGCGAAACGAGAGTCCCTGAATGCCAGATTTGAGATG 361
QY 422 CCTCTGATGAAGCGCGCGGCTTGGGCTGTGAAGTCTTCCGTTACGAATTCAGAGATT 481
DB 362 CCATCAACCAAGCTGCTGACTGCTGGGCTATCCGCTGCTCCGTTATGATGATCAAGATA 421
QY 482 TGGTTCGCGCAGAAATTCCTTGGCGGATGACGAGCAAAATTACCGCGCAAGCGCAAA 541
DB 422 TCCATGTGCAACCGCGGCTGAAAGATGTAATGACATGAGTGAAGCAGAGCGCGCA 481
QY 542 AACGCGCCGATATGCGCAATCCGAAGCCGTAATGAAATCAATCAATCACTTGCAGTG 601
DB 482 AACGCGCCAGATTCAGATCTGA-----GG 508
QY 602 GTACAGCTGAAGCGCAATTCGAATCCGAAGCGAGGCTCAGGCTCGGCTCAATGCT 661
DB 509 GGAACCGAGATCGGCTCATATGTGAGCAAGGAGAAACAGGCCCAAGATCTCGGCT 568
QY 662 CCAATGCGGAGAAATGCGCGCATCAACCGCGCAAGCGAAGCGGAATCCCTGCGC 721
DB 569 CCGAAGCAGAAAGGCTGAACGATTAATCAAGGACGAGAGAGCCAGTCAATTTCTG 628
QY 722 TTGTTCCGAAGCCATCCGAAGCATCCGTAATTTGCGCGCCCTTGAACCCAG 781
DB 629 CGAAGCGCAAGGCTTAAGCTTAATTTGAAATCTGGCTGAGCTTGAACAACTA 688
QY 782 GCGGCGCGATGCGGCTCATCTGAAGATTGGGAACTAGTACGCGCGCTTCAACATC 841
DB 689 ATGAGATGACGAGCTTCACTGACTGTGCGCGAGAGTATGTCAAGCGCTTCTCAAC 748
QY 842 TTGCGAAGAAAGCAATAGCTATATGTCGCGCAATGTTGCGGACATCGGAGCTGA 901
DB 749 TGGCGAAGACTCCACACTATCTACTGCTCCCAACCTGGGATGTCAACGAGATG 808
QY 902 TTTCTGCGCGCATG 915
DB 809 TGGCTCAGGCGCATG 822

RESULT 11
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LOCUS BUS08142
DEFINITION AGENCOURT 10128235 NIH_MGC_71 Homo sapiens cDNA IMAGE:6502173
ACCESSION BUS08142
VERSION BUS08142.1 GI:22814375
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1095)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straube, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
Plate: LMNL4057 Row: m Column: 22
High quality sequence stop: 760.
Location/Qualifiers
1..1095
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN
Query Match 16.4%; Score 155.6; DB 5; Length 1095;
Best Local Similarity 50.6%; Pred. No. 5.6e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGCAGAAATCCACGTTGTCGAAAGGCTGGGCGTTTCCATGCGCCCTGA 121
DB 12 TCGTCCCGCAGCAGAGGCTGGGCGTTGTCGAAAGGCTGGGCGTTTCCATGCGCCCTGA 71
QY 122 CGGCGCGTTGAATTTTGAATTCCTTATCGAACCGGCTGCCATCCGCGCATTCGCTGA 181
DB 72 AGCTGTTGGAATCATCTCTGTTAGAACCGGATCCGATATGTCAGAGTCTCA 131
QY 182 AAGAAATCCTTTAGAGTACCGACGAGCTGTCATCAGCGGATTAATACGAATTGA 241
DB 132 AGGAAATGTCATCAAGCTGCTGAGCAATGCGCTGACTCTGACATGTAATCTCTGC 191
QY 242 CTGTTGAGCGCATCTATTTTCCAGTAACGATCCCAATTCGCTCATACGTTTGA 301
DB 192 AAATGATGAGTCTTTTACCTGCGCATGAGACCTTCAAGGCAAGCTAGCTGTG 251
QY 302 GCAATCAATTAATGCAATTAACGATGCGCAAGAGAGCTGCTTCTGTTATGCGGC 361
DB 252 AGGACCTGAGTATGCGGCTCAACGAGTCAACCAACCATGATGAGAGCTCGCA 311
QY 362 GTATGAGTTGGAAGAAAGCTTGAAGACGCGCAAGAAATCAACATACGCTGCTCG 421
DB 312 AACTCTCTGAGAAAGTCTTCGCGAAGGAGTCTGATATCCAGATGTGGATG 371
QY 422 CCTCTGATGAAGCGCGCGGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGATT 481
DB 372 CCATCAACAAAGCTGCTGAGCTGTGGGTTCCGCTGCTCCGTTATGATGATCAAGATA 431
QY 482 TGGTTCGCGCAGAAATTCCTTGGCGCAATGACGCAAAATTAACCGCGAAGCGAAA 541
DB 432 TCATGTGCAACCGCGGCTGAAGAGTCTATGACAGATGAGTGAAGCGAGCGCGCA 491
QY 542 AACGCGCCGATATGCGCAATCCGAAGCGGTAATGAAATCAACATCACTTCCAGTG 601
DB 492 AACGCGCCAGATTCAGATCTGA-----GG 518

QY 602 GTACGCTGTAAGCCGGAATTCACAAATCCGAAGCGGCTCAGGCTGCGGTCATATGCGT 661
DB 519 GACCCCGAGATCGCCCTCATATGTGGCAAGAAAGGAAACAGGCGCCAGATTCCTGGGCTT 578
QY 662 CCAATGCGCGAAGAAATCGCCGTCATCAACCGCGCAAGCGGAAGCGGAATCCCTGCGCC 721
DB 579 CCGAAGCGAAGAAAGGCTGAACGATTAATTCAGCGACGAGAGAGGCGCATGCAAGTTCTGG 638
QY 722 TTGTTGCCGAAGCCCAATGCGGAAGCCATCCGTCAAAATGCGCGCCCTTCAACCCAG 781
DB 639 CGAAGCGCAAGGCTTAAGCTGAAGCTATTCGAATCCTGGCTGCAAGCTCTGACACAACATA 698
QY 782 GCGGGCGGATGCGGTCATCTGAAGATTGGCGAATACGTACCGCGCTTCAACATC 841
DB 699 ATGAGATGACAGACACTTCACTGACTGTGGCGGACAGATATGTCAGCGGTTCTCAAC 758
QY 842 TTGCGAAGAAAGCAATACGCTGATTATGCGCGCAATGTTGCCGACATCGGACCTGA 901
DB 759 TGGCCAGGACTCCACACACTATCTCTACTGCTCCCAACCTGGCGATGTCAACGACATG 818
QY 902 TTTCTGCGCGCATG 915
DB 819 TGGCTCAGGCCATG 832

RESULT 12
CR612088 1103 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DJ011YA06 of T cells (Jurkat cell line)
DEFINITION Cct 10-normalized of Homo sapiens (human).
ACCESSION CR612088
VERSION CR612088.1 GI:50492895
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1103)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifeitech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1103)
Genoscope.
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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1. 1103
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/db_xref="taxon:9606"
/clone="CS0DJ011YA06"
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10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 16.4%; Score 155.6; DB 3; Length 1103;
Best Local Similarity 50.6%; Pred. No. 5.6e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
QY 62 TCATCCCGACAGAGAAATGTCACGTTGTGGAAGGCTGGGGGTTTCCATCGCGCCCTGA 121
DB 43 TGTGTCGACAGAGAGGCTGGGTGTGTGAGCGAATGAGCCGATTCCACCGGATCTGG 102

QY 122 CGGCGGTTGATATTTTGAATTCCTTATTCAGACCGGCTGACCTACCGCATTCGCTGA 181
DB 103 AGCTGGTTTGAACATCTCTATCCCTGTGTGTAAGACCGGATTCGATATGTGACAGTCTCA 162
QY 182 AAGAAATCCCTTTAGACGTACCGACGAGGTCTGATCAGCGCGATTAATACGAATTTGA 241
DB 163 AGGAAATGTATCAAGGTGCTGAGAGAGTGCGGTGTGATCTCTGCAATATTAATCTGCG 222
QY 242 CTGTGACGATCATCTATTTCAGATTAACCGATCCAACTGGCCCTCATACGTTTGA 301
DB 223 AAATCGATGGAATCCTTACCTGCGCATCAAGACCTTCAAGGCAAGCTACGCTTGG 282
QY 302 GCAACTATATATGCAATTATCCGACTTGCACAAAGACGCTGCTCCGTTATCGGAC 361
DB 283 AGGACCTGATATGCTGCTACCCAGCTAGCTCAAAACATGATGATCAAGCTCGGCA 342
QY 362 GTATGAGTTGGAACAAACGTTTGAAGAACGCAAGCAATCAACAGTACGCTGCTCG 421
DB 343 AACTCTCTGTGACAAAGTCTTCGCGGAAACGAGGTCCCTGAATGCCAGATTGTGATG 402
QY 422 CCTTCGATGAAGCGCGCGCTTGGGTGTGAAGTCTTCCGTTACGAATCAAGATT 481
DB 403 CCATCAACCAAGCTGCTGATGCTGGGTATTCGCTGCTCCGTTATGATCAAGATGA 462
QY 482 TGTTCGCGCCCGCAAAATTCCTTGGCGGATGAGGACCAAAATTACCGCGCAACGCAAA 541
DB 463 TCCATGTGTCACCCCGGTGAAGAGTCTTATGACAGATGAGTGAGAGGACGCGGCA 522
QY 542 AACGCGCCGATATGTCGCAATCCGAAGGCGTAAATGCAAAATCAACTTGCAGATG 601
DB 523 AACGCGCCAGCTTTAGATGCTGA-----CG 549
QY 602 GTACGCTGAAAGCGGAATTCACAAATTCGAAGCGGAGCTCAGGCTGCTCAATGCGT 661
DB 550 GGAACCGAAGTGGCGCATCAATGTGGCAGAAAGGAAACACAGGCCAGATCTGCGCT 609
QY 662 CCAATGCGCGAAGAAATTCGCCGATCAACCGGCAAGGCGAAGCGGAATCCCTGCGCC 721
DB 610 CCGAAGCGAAGAAAGGCTAAACGATTAATCAGGCGACGAGAGAGGCGAGTCAAGTTCTGG 669
QY 722 TTGTTGCCGAAGCCCAATGCGGAGCCATCCGTCAAAATGCGCGCCCTTCAACCCAG 781
DB 670 CGAAGCGCAAGGCTTAAGCTGAAGCTATTCGAATCTGCTGACACTCTGACACAACATA 729
QY 782 GCGGGCGGATGCGGTCATCTGAAGATTGGGGAACATACGTACCGCGCTTCAACATC 841
DB 730 ATGAGATGACAGACACTTCACTGACTGTGGCGGACAGATATGTCAGCGGTTCTCCAAC 789
QY 842 TTGCGAAGAAAGCAATACGCTGATTATGCGCGCAATGTTGCCGACATCGGACCTGA 901
DB 790 TGGCCAGGACTCCCAACACTATCTTACGCTCCCAACCTGGCGATGTCAACGACATG 849
QY 902 TTTCTGCGCGCATG 915
DB 850 TGGCTCAGGCCATG 863

RESULT 13
CR614697 1142 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DJ012Y2P1 of T cells (Jurkat cell line)
DEFINITION Cct 10-normalized of Homo sapiens (human).
ACCESSION CR614697
VERSION CR614697.1 GI:50495504
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1142)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue
REFERENCE 2 (bases 1 to 1142)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1142
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ012YK06"
/tissue_type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 16.4%; Score 155.6; DB 3; Length 1142;
Best Local Similarity 50.6%; Pred. No. 5.6e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCCAGAGAGATCCAGTGTGCGAAGGCTCGGGGTTTCATGCGCCCTGA 121
Db TCGTCCCGGAGAGAGGCTCGGGTGTGAGACCAATGGCCGATTCCACCGGATCTCG 168
Qy CGGCGGTTTGAATATTTGATCCCTTATCGACCGCGTCCCTACCGCATTCGTGA 181
Db AGCCTGTTTGAATCCTCATCCCTGTGTAGACCGATCGAATATGTGAGAGTCTCA 228
Qy 122 CGGCGGTTTGAATATTTGATCCCTTATCGACCGCGTCCCTACCGCATTCGTGA 181
169 AGCCTGTTTGAATCCTCATCCCTGTGTAGACCGATCGAATATGTGAGAGTCTCA 228
182 AAGAAATCCCTTATGAGATCCACCGAGTGTGATCAGCGCGATTAATACGAATGA 241
Db AGGAATATGTCATCAACGTGCTGAGAGTGGCTGTACTCTCGACATGTAATCTGTC 288
Qy 229 AGGAATATGTCATCAACGTGCTGAGAGTGGCTGTACTCTCGACATGTAATCTGTC 288
242 CTGTGACGGCATCATATTTCAAGTAAACGATCCCAACTCCCTCATACGGTTGCA 301
Db AATATGATGAGATCTTTTACCTGCCATCATGACCTTTCAAGGCAAGCTACGTTGG 348
Qy 289 AATATGATGAGATCTTTTACCTGCCATCATGACCTTTCAAGGCAAGCTACGTTGG 348
302 GCACATCATTAATGCAATTAACCGACTTCCCAAGACGCTGCTTCCGTTATCGGAC 361
Db AGGACCTGAGATGCTCGTCAACCGACTGCTCAACCAACATGATCAGAGCTCGGCA 408
Qy 349 AGGACCTGAGATGCTCGTCAACCGACTGCTCAACCAACATGATCAGAGCTCGGCA 408
362 GTATGAGTTGAGCAAAACGTTTGAAGAACGAGCAAAATCAACAGTACCGTCTCG 421
Db AACTCTCTGTGACAAAGTCTTCCGGAACGAGAGTCCCTGAATCCAGCATTTGATG 468
Qy 422 CCCTGATGAGAGCGCGCGGCTTGGGGTGAAGTCTCCGTTACGAAATCAAGATTT 481
469 CCATTAACCAAGCTGTGATCTGCTGGGATTCGCTGCTTCCGTTATGATCAAGGATA 528
Qy 542 TGGTTCGCGCGAAGAAATCTTTCGCGCATGCAAGCAAAATTAACCGCGAAGCGGAA 541
589 AACGGGCGCACAGTTCTAGAGTCTGA-----G 615
Db 602 GTCAAGCTGGAAGCCGAATCCCAATCCGAGAGGAGGCTGAGGCTGGCGATTCGCT 661
Qy 616 GAGACCCGAGAGTGGCGCATCAATGTGGCAAGAGGAGAAACAGGCCCAAGTCTGGCCT 675
Db 662 CCAATGCGGAGAAATTCGCCCGCATCAACCGCGCAAGGCGAAGCGGATTCCTCGCC 721
Qy 676 CCGAAGCGAAGAAAGCTGAACAGATTAATCAAGCGAGAGAGGCGAGTGTGAGTTCGG 735

Qy 722 TTGTTCGGAAGCAATGCGAAGCCATCCGTCAAAATGGCCGCCCTTCAAAACCAAG 781
Db CGAAGCGCAAGCTTAAGCTGAAGGATATTGAAATCCGTGGCTGAGGCTTGACACATGA 795
Qy 782 GCGGGCGGATGCGGTCAATCTGAATGTCGGGAAACATACGTAACCGCGCTTCAACATTC 841
Db ATGAGATGACAGAGCTTTCATGATGTGGCCGAGAGTATGTACAGCGCTTCCAAAC 855
Qy 842 TTGCGAAGAAAGAAATAGCTGATTAATGCCCGCAATGTTGCGCATCGGAGCGCTGA 901
Db TGGCAAGAGACTCCAAACATATCTACTGCTTCAACCTTGCGAGTCAACAGCATGG 915
Qy 902 TTTCTGCGGCGCATG 915
Db 916 TGGCTCAGGCCATG 929

RESULT 14
CR625020 1196 bp mRNA linear HTC 21-JUL-2004
LOCUS
DEFINITION full-length cDNA clone CS0DJ012YK06 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).
ACCESSION CR625020
VERSION CR625020.1 GI:50505827
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1196)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue
REFERENCE 2 (bases 1 to 1196)
Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1196
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ012YK06"
/tissue_type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 16.4%; Score 155.6; DB 3; Length 1196;
Best Local Similarity 50.6%; Pred. No. 5.7e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCCAGAGAGATCCAGTGTGCGAAGGCTCGGGGTTTCATGCGCCCTGA 121
Db TCGTCCCGGAGAGAGGCTCGGGTGTGAGACCAATGGCCGATTCCACCGGATCTCG 192
Qy 122 CGGCGGTTTGAATATTTGATCCCTTATCGACCGCGTCCCTACCGCATTCGCTGA 181
Db 193 AGCCTGTTTGAATCCTCATCCCTGTGTAGACCGAGTCCGATATGTGAGAGTCTCA 252
Qy 182 AAGAAATCCCTTATGAGATCCACCGAGTGTGATCAGCGCGATTAATACGAATGA 241

Db 253 AGGAAATTGATCAAGGCTGAGCAGTGGGCTGTGACTCTGACATGTAACCTGCG 312
 Qy 242 CTGTTGACGGCATCATTAATTTCCAGTAACCGATCCCAACTCCCTCATACGGTTGA 301
 Db 313 AAATGATGAGTCTTTAAGTCCGATCATGACCTTTACAAAGGCAAGCTACGGTGTGG 372
 Qy 302 GCAATACATTAATGCAATTAACCGCTTGGCCCAAGCGCTGGTCCGTTACGGGC 361
 Db 373 AGGACCTGAGTATCCGCTGACCTGAGTAAAGCTGCAAGCAATGAGTACAGCTGGCA 432
 Qy 362 GTATGAGTATGGAACAAAGCTTTGAAAGCGGAGCAATCAACAGTACCGTCTCG 421
 Db 433 AACTCTCTGACAAAGTCTTCCGGGAAGGGAAGTCCCTGATGCGCAGATTTGGATG 492
 Qy 422 CCTTGATGAAAGCCCGGGGCTTGGGCTGGAAGTCTCTCGTTACGAATTCAGAT 481
 Db 493 CCATCAACCAAGCTGCTGCTGAGGATCCGCTGCTCGCTGCTGATGAGTCAAGAT 552
 Qy 482 TGGTCCCGCCGGAAGAAATCCTTCCGCAATGCAAGCAATTAACCGCCGGAAGAA 541
 Db 553 TCCATGTGCGACCCCGGGTGAAGAGTCTATGCAAGTGAAGTGAAGCGAGCGCGGA 612
 Qy 542 AACGGCCCGTATTTGCGGCAATCCGAAGCGCTAAATCGAACAATCAACTTGGCAATG 601
 Db 613 AACGGCCCAAGTTCTAGAGTCTGA-----GG 639
 Qy 602 GTACGCGTGAAGCCGAATTCACAATCCGAAGCGGAGCTCAGGCTGCGTCAATGCT 661
 Db 640 GGAACCGAAGTCCGCGCATCATGTGCGAAGGGAAGAAACAGGCCAGATCTGGCCT 699
 Qy 662 CCAATGCCGAAGAAATCCCGCGCATCAACCGCGCCAAAGCGAAGCGGAATCCCTGCGC 721
 Db 700 CCGAAGCAAGAAAGGCTGAACAGATTAATCAGGCAAGCAAGAGCGCAATGAGTCTGG 759
 Qy 722 TTGTTGCGGAAGCAATGCGAAGCATCGCTCAATTTGCGCGCGCTTCAACCCGAAG 781
 Db 760 CGAAGGCCAAGGCTAAAGCTTAAGCTTAATCTGCTGCTGAGCTTGAACCAATGA 819
 Qy 782 GCGGGCGGATCGGCTCAATCTGAAGATTTGCGGAACATACGTAAGCGGTTCAACATC 841
 Db 820 ATGAGATGCAACAGCTTCACTGATGCTGCGGAGAGATATGACGCGGTTCTCCAAC 879
 Qy 842 TTGCGAAGAAAGCAATACGCTGATTAATGCGCGCCCAATTTGCGCGCATCGGCAAGCTGA 901
 Db 880 TGGCGAAGGACTCAACACTATCTACTGCTCCCTCCAACTGCGGATGACACGATG 939
 Qy 902 TTTCTGCGCGCATG 915
 Db 940 TGGCTCAGGCGCATG 953

RESULT 15
 CR610520 1199 bp mRNA linear HTC 21-JUL-2004
 LOCUS Full-length cDNA clone CS0D008YL10 of T cells (Jurkat cell line)
 DEFINITION CR610520
 Cot 10-normalized of Homo sapiens (human).
 ACCESSION CR610520
 VERSION CR610520.1 GI:50491327
 KEYWORDS HTC; CDSUT; cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1199)
 AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polyes, D.
 JOURNAL Full-length cDNA libraries and normalization
 REMARK Unpublished
 Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 2 (bases 1 to 1199)
 REFERENCE Genoscope.
 AUTHORS Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="CS0D008YL10"
 /cissue_type="T cells (Jurkat cell line) Cot
 10-normalized"
 /plasmid="pCMVSPORT_6"
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 Query Match 16.4% Score 155.6; DB 3; Length 1199;
 Best Local Similarity 50.6% Pred. No. 5.7e-35;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
 Qy 62 TCATCCCCAGAGAGATCCACGTTGTGAAAGCTCGGCGTTTCATCGGCCCTGA 121
 Db 142 TCGTCCCGCAGAGAGAGGCTGGGTGTGAGCGAATGGGCGGATTCACCGGATCTGG 201
 Qy 122 CGGCGGTTTGAATTTTGAATTCCTTTATGACCGGCTGCTTACCGCATTCGCTGA 181
 Db 202 AGCTGGTTGAACATCTCATCTCCTGTGTGAGCCGATCCGATATGTCAGAGTCTCA 261
 Qy 182 AAGAAATCCCTTAAAGTACCCAGCGAGTGTGATCAGCGCGATATAGCAATTGA 241
 Db 262 AGGAAATGTCACTCAACGCTGTGAGAGTGGCTGTGATCTTCAATGTAATCTGCG 321
 Qy 242 CTGTTGACGGCATCATTAATTTCCAGTAACCGATCCCAACTCCCTCATACGGTTGA 301
 Db 322 AATGATGAGTCTCTTTACCTGCGCATATGAGACCTTTACAGACCAAGTACGGTGG 381
 Qy 302 GCACTACATTAATGCAATTAACCAAGCTTCCCAAGCAAGCGTGGCTTCTGTTATGGCG 361
 Db 382 AGGACCTGAGTATCCGCTCAACCGCTAGCTAGCTCAACCAACATGAGATCAGAGCTGGCA 441
 Qy 362 GTATGAGTGTGACAAACGTTTGAAGACGGAAGAAATCAACAGTACCGTCTCGG 421
 Db 442 AACTCTCTGGAACAAAGTCTTCCGGAACGGAAGTCCCTGATGACGACATTTGGATG 501
 Qy 422 CCTGATGAGAGCGCGCGGCTTGGGGTGAAGTCTCCGTTACGAATCAAGAT 481
 Db 502 CCATCAACCAAGCTCTGATGCTGCGGATATCCGCTGCTCCGTTATGATCAAGATGA 561
 Qy 482 TGGTCCGCGCAAGAAATCCTTCCGCAATGCAAGCAATTAACCGCCGAAGCGGAA 541
 Db 562 TCATGATGCAACCGCGGTGAAGAGTCTATGCAATGAGTGAAGGAGGCGGCGGA 621
 Qy 542 AACGGCCCGTATTTGCGCGAATCGAAGCGCTGAATGAACAATCAACTTGGCAATG 601
 Db 622 AACGGCCCAAGTTCTAGAGTCTGA-----GG 648
 Qy 602 GTACGCTGAAGCCCAATTCACAATCGGAAGGCGAGGCTCAGGCTGCGTCAATGCGT 661
 Db 649 GGAACCGAAGTCCGCGCATTAATGCGCAAGAGGGAAGAAACAGGCCAGATCTGGCCT 708
 Qy 662 CCAATGCCGAAGAAATCCCGCGCATCAACCGCGCAAGGCGAAGCGAATCCCTGCGCC 721
 Db 709 CCGAAGCAAGAAAGGCTGAACAGATTAATCAGGCAAGGAGAGAGGCAAGTCAAGTCTGG 768
 Qy 722 TTGTTGCGAAGCAATGCGAAGCATTCGTAATTTGCGCGCGCTTCAACCCGAAG 781
 Db 769 CGAAGGCCAAGGCTAAAGCTGAAGCTATGCAATCTGCTGCTGACATCAACATGA 828
 Qy 782 GCGGGCGGATCGGCTCAATCTGAAGATTTGCGGAACATACGTAAGCGCGGTTCAACATC 841

Db 829 ATGAGATGCGACGACTTCACTGACTGTGGCCGAGCAGATATGACGCGCTTCTCCAAAC 888
Qy 842 TTGGCAAGAAAGAAATCGCTGATTTATGCGCGCAATGTTGCGGACATGGGACGCCGA 901
Db 889 TGGCGAAGACTCCAACTACTACTGCTGCTCCACCTGGGAGATGTACACGACATGG 948
Qy 902 TTTCTGCGCGCATG 915
Db 949 TGGCTCAGGCCATG 962

RESULT 16
CR608510 1206 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DK006YK04 of Hela cells Cot 25-normalized
DEFINITION
ACCESSION CR608510.1 GI:50489317
VERSION CR608510.1
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1206)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue
Genoscope.
2 (bases 1 to 1206)
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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/db_xref="taxon:9606"
/clone="CS0DK006YK04"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 16.4%; Score 155.6; DB 3; Length 1206;
Best Local Similarity 50.6%; Fred. No. 5.7e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

Qy 62 TCATCCCCCAGAGGAATGTCACGCTGTCGAAGGCTGGGCGTTTCATGCGCCCTGA 121
Db 142 TCGTCCCGCAGAGAGAGCTGGGCTGGAGCGCAATGGCCGATTCCACCGGATCTGG 201
Qy 122 CGGCGGTTTGAATTTGATTCCTTTATCGACCGCGTGCCTACCGCATTCGCTGA 181
Db 202 AGCGTGTTTGAATCTCATCTCCTGTGTTAGACCGGATCGATATGTGACAGATCTCA 261
Qy 182 AAGAAATCCCTTTAGACGTACCCAGCGGCTGTCATACGCGGATTAATACCAATGA 241
Db 262 AGGAATTTGTATCACTACGCTGTGAGCGGTGTACTCTCGACAAATTAATCTGTC 321
Qy 242 CTGTTGAGGAGCATCTATTTCGAAGTACCGAATCCGAATCGCTCATACGGTTGA 301
Db 322 AAATGAGAGAGTCTTTTACCTGCGCATATGAGACCTTACAGGCAAGCTACGGTGG 381
Qy 302 GCAACTATATTGAGCAATTAACCGACTTGGCCAAACGACGCTGCGTTCCGTTACGGGC 361

Db 382 AGGACCTGAGTATGCCGTACACCCAGTACTCAACCAACATGATATCAGAGCTCGGCA 441
Qy 362 GTATGAGATTGACAAACAGTTTGAAGACGCGCAATTAACAGTACCGTCTCCG 421
Db 442 AACTCTCTCTGACAAAGTCTTCCGGGAAAGGAGTCCCTGAAATGCCAGATTTGGATG 501
Qy 422 CCTGATGAAGCCGCCGCGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATT 481
Db 502 CCATCAACCAAGCTGTGTAAGTGTGGGATATCCGCTCTCCGTTATGATATCAAGGATA 561
Qy 482 TGGTTCGCGCGCAAGAAATCTTCCGCAATGCGAGCAAAATTAACCGCGGAAGCGGAA 541
Db 562 TCCATGTGCCACCCCGGATGAAGAGTCTATGACATGAGGTGAGAGCGAGCGCGGA 621
Qy 542 AACGCGCCGATATGCGGAATCCGAAGCGCGTAATATCGAACAAATCAACTTCCCATG 601
Db 622 AACGGGCAAGTTTCTAGAGTCTGA-----GG 648
Qy 602 GTGAGCGTGAAGCCGAATCCAAATCCGAAGCGAGGCTCAGCGTGCCTCAATCGT 661
Db 649 GACCCGAGAGTCCGCCATCAATGTGCGAGAGGGAAGAAACAGGCCAGATCTGGGCT 708
Qy 662 CCATGCGGAGAAATGCGCGCATCAACCGCGCAAGCGGAAGCGGAATCCTGGGCC 721
Db 709 CCGAAGCAGAAAGAGCTGAACAGTAAATCAGGACGAGAGAGGCAAGTGCAGTCTGG 768
Qy 722 TTGTTGCGAAGCCATGCGGCAAGCCATCCGTCAAATTGCGCGCGCTTCAACCAAG 781
Db 769 GGAAGGCGCAAGCTTAAGCTGAATTTGGAATCTGCGCTGACGCTCTGACACAACTA 828
Qy 782 GCGGGGCGAGTGCCTGATCTGAAGATTGCGGAACAATACGTAGCGCTTCAACAATC 841
Db 829 ATGAGATGACGACGACTTCACTGCTGTGGCCGACGATATGTCAAGCGCTTCCAAAC 888
Qy 842 TTGCGCAAGAAAGAAATACGCTGATTATGCGCCCAATGTTCCGATCGGCGCTGA 901
Db 889 TGGCGAAGAGCTCCAACTACTACTGCTCCAAACCTGGGAGTGTACCGAGATGG 948
Qy 902 TTTCTGCGCGCATG 915
Db 949 TGGCTCAGGCCATG 962

RESULT 17
CR592181 1208 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DC005YF20 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CR592181
VERSION CR592181.1 GI:50472988
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1208)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradey Avenue
Genoscope.
2 (bases 1 to 1208)
REFERENCE Direct Submission
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

SOURCE

Location/Qualifiers
1. 1208
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC005YR20"
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/plasmid="PCWSPORT_6"

ORIGIN

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Query Match      16.4%; Score 155.6; DB 3; Length 1208;
Best Local Similarity 50.6%; Pred. No. 5.7e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
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62 TCATCCCCCAGAGAGATCCAGTTCGAAAGGCTCGGGGCTTTCATCGCCCTGA 121
 142 TCGTCCGACAGAGAGGCTGGGTGTGAGAGCAATGGCCGATTCACCGGATCTGG 201
 122 CGGCGGTTGAATTTTGAATCCCTTTATCGACCGGCTGCCCTACCGCCATTCGCTGA 181
 202 AGCGGTGTTGAATCTCTCACTCCCTGTGTAGACCGGATCGATATGTGACAGATCTCA 261
 182 AAGAAATCCCTTTAGACGTAACCCAGGCTGATCAGCGGCGATATAGCAATTGA 241
 262 AGGAATTTGATCAACGCTGCTGACAGTGGCTGTGACTTTCGACAAATGTAATCTTGC 321
 242 CTGTTGACGCAATCATTTATTTCAAGTAACCGATCCGAACTCCCTCATACGCTTGA 301
 322 AAATGATGAGATCTTTACCTGCCCATCATGAGACCTTTACAGGCAAGTACGCTGAG 381
 302 GCAACTACATTATGAGCAATTAACCAAGCTTCCCAACGACGCTGCTTCCTTATCGGAC 361
 382 AGGACCTGAGATATCCCTCAACCCAGCTAGCTCAACCAACATGAGATCAGAGCTGCA 441
 362 GTATGAGATTTGAGCAAAACGTTTGAAGAACGGAATCAACAGTACCGCTCTCG 421
 442 AACTCTCTGAGCAAAAGCTTTCGAGGAAAGGAAAGTCCCTGATGACGATTTGTGATG 501
 422 CCCTGATGAAAGCCCGGCGCTTGGGTGTGAAAGTCTCCCTTACGAAATCAAGAT 481
 502 CCATACCAACAGCTGTGATCTGCTGGGTATCCGCTGCTCGTTATGATGATCAAGATA 561
 482 TGGTCCGCGCAAGAAATCTTTCGCGCAATGACGACAAATTAACCGCCGACCGGAA 541
 562 TCCATGTGCAACCCGCGGAGAAAGATGATGACATGACGCTGAGGACGACGCGCA 621
 542 AACGCGCGCTATTTGCCGAATCCGAAGGCGCTAAATCAACAACTTGGCAATG 601
 622 AACGCGCCACAGTTCTAGAGTCTGA-----GG 648
 602 GTGAGGTGAAAGCCGAAATCCAAATCCGAAGGCGAGGCTGAGCTGCGTCAATGCGT 661
 649 GAAACCCGAGAGTCCGATCAATATGAGCAAGAAAGGAAAGAAAGCCGACGATCTGGCCT 708
 662 CCATATCCGAGAAATTCGCCGATCAACCGCGCAAGGCGAAGCGAATCTTGGCGCC 721
 709 CCGAAGCAAGAAAGGCTGAAGATTAATCAGGACAGAGAGGCGAGTCAAGTCTGG 768
 722 TTGTTGCGAAGCAATGCGCAAGCATCCGTCAAAATTCGCGCGCTTCAAAACCAAG 781
 769 CGAAGGCTCAAGGCTAAGCTGAAGCTATTCGAATCTGCTGAGAGCTGACCAACATA 828
 782 GGGGGGCGATGGGCTCAATGGAAGATTGCGGAAATATACGTAGCGGCTTCAACATC 841
 829 ATGGAATGCAAGACCTTCACTGACTGTGGCGAGAGATATGTCAGCGGCTTCCAAAC 888
 842 TTGCAAAAGAAAGCAATAGCTGATTAATGCGCGCAATGTTGCGGATCGGACGCTGA 901
 889 TGGCCAAAGATCTCAACATATCTTACTGCTTCAACCTGGCGATGTCACCAAGATGG 948
 902 TTTTCTCCGCAATG 915
 949 TGGCTCAGGCAATG 962

RESULT 18

LOCUS

AF161458 1218 bp mRNA linear HTC 22-MAY-2001
 Homo sapiens HSPC108 mRNA, complete cds.

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORIGIN

```
Query Match      16.4%; Score 155.6; DB 3; Length 1218;
Best Local Similarity 50.6%; Pred. No. 5.8e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
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62 TCATCCCCCAGAGAGATCCAGTTCGAAAGGCTCGGGGCTTTCATCGCCCTGA 121
 94 TCGTCCGACAGAGAGGCTGGGTGTGAGAGCAATGGCCGATTCACCGGATCTGG 153
 122 CGGCGGTTGAATTTTGAATCCCTTTATCGACCGGCTGCCCTACCGCCATTCGCTGA 181
 154 AGCTGCTTGAATCTCTCACTCCCTGTGTAGACCGGATCCGATATGTCAGAGATCTGA 213
 182 AAGAAATCCCTTTAGACGTAACCCAGGCTGATCAGCGGCGATTAATAGCAATTGA 241
 214 AAGAAATTTGATCAACGCTGCTGAGAGTGGCTGTGACTTTCGACAAATGTAATCTTGC 273

FEATURES

SOURCE

1. 1218
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CBCAPB12"

/cell_type="cd34+ stem cells"

/issue_type="blood"

18.1046

/codon_start=1

/product="HSPC108"

/protein_id="AAF29073.1"

/translation="MRGSLASGRACRASSGAPRTVTVLVFVPOEAMVVERMGRFRI

LEPGNITILPILDRIRRYQSLKEIYINPPOGSAATLDVITLQIDVILYLRIMDPKAS

YGEDEPEYAVTQLAQTTRSEIKSLDKTFRRESLNASLYDAINQADCGIRICAR

YEIKDIHVPPRYKSMQVABERKRRTLVSEBSTRSALINAVAGKQAOYLASBAE

KAEOINQAGASAVLAKAKAKAELIRIAALTDHNDPAASLTVAOQYSAFSEKLA

KDSNTILPLPSNGDVTSMVAQMGVYALTAAPVGTDPDLSGSSRDVQGTDAISLDE

ELDRVYMS"

ORIGIN

```

Qy 242 CTGTTGACGCAATCTATTTCAGATACCGATCCAAACTCGCTTACATCGGTTGCA 301
Db 274 AAATGATGAGAGTCTTTACCTGCGCCATCATGAGACCTTACAGGCAAGCTTACGGTGG 333
Qy 302 GCAACTATATATGAGCAATTAACCGAGCTTGGCCAAAGACGCTGGCTTCCGTTATCGGGC 361
Db 334 AGGACCTGAGTAGTCCGCTCAACCCAGCTAGCTCAAAACAACATGAGTACAGAGCTCGCA 393
Qy 362 GTATGAGTTGAGACAAACGTTTGAAGACGCAAGAAATCAACATACCGTCTGCTCCG 421
Db 394 AACTCTCTGAGCAAAAGTCTTCCGGGAACGGAGATCCCTGAATGCCAGATTTGGATG 453
Qy 422 CCTTCGATGAAGCCCGCGGCTTGGGGTGTGAAGTCTCTCCGTTACGAAATCAAGATT 481
Db 454 CCATCAACCAAGCTGCTGACTGTGGGGTATCCGCTGCTCGTTATGAGATCAAGGATA 513
Qy 482 TGGTTCCGCGGCAAGAAATCTTGGCGCAATGCAAGGCAAAATTAACGCCGCAAGCGGAA 541
Db 514 TCCATGTGCCAACC CGGGTGAAGAGTATTGACAGATCAGGTGAGGCAAGCGCGGA 573
Qy 542 AACGCGCCGTAATTGCGCAATCCGAAGGCGTAAATGAAATCAACATCAACCTTGCAAGT 601
Db 574 AACGCGCCAGATTCAGATCTGAAGTCTGA-----GG 600
Qy 602 GTCAAGCGTGAAGCCGAAATCCAAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCGT 661
Db 601 GAGCCCGAGAGTCCGCGCATCATGTGCGAGAGGGAAGAAACAGGCCAGATCTCGGCT 660
Qy 662 CCAATGCCGGAAGAAATCGCCCGCATCAACCGCGCAAGGGAAGGGAATCCCTCGGCC 721
Db 661 CGAAGCGAAGAAAGGCTGAACAGATTAATCAAGGAGGAGGAGGCAAGTCAAGTTCTGG 720
Qy 722 TTGTTGCCGAAGCCATGCCGAGCCATCCGTTCAATTTGCGCGCCCTTCAAAACCCAG 781
Db 721 CGAAGCGCAAGGCTTAAGCTGAAGTATTCGATCTCTGCGCTGCACTGACAGCACTA 780
Qy 782 GCGGGCGGAGTCCGCTCAATGTGAAGATGCGGAACAAATCAATGACCGCTTCAACATC 841
Db 781 ATGAGATGACAGAGCTTCACTGACTGTGCGGAGCATATGTACGCGCTTCCAAAC 840
Qy 842 TTGCGCAAGAAAGCAATCGCTGATTAATGCGCCCAATGTTCCGACATCGGACCTGGA 901
Db 841 TGGCGCAAGAGCTCCAAACATATCTTCTGCTCCACCCCTGGGATGTCAACAGCATG 900
Qy 902 TTTCTGCGCGCATG 915
Db 901 TGGCTCAGGCGCATG 914

RESULT 19
CR591719 1532 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODK005YE05 of Hela cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR591719
VERSION CR591719.1 GI:50472526
KEYWORDS HTC; CNS1 cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1532)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
Genoscope,
2 (bases 1 to 1532)
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

```

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COMMENT
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Source
1. 1532
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK005YE05"
/issue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 16.4%; Score 155.6; DB: 3; Length 1532;
Best Local Similarity 50.6%; Pred. No. 6.2e-35;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
Qy 62 TCATCCCCCAGAGAGATCCAGTTCGAAAGGCTCGGAGCTTTCATGCGCCCTGA 121
Db 141 TCGTCCGCGAGAGAGGCTCGGAGTGTGAGAGCAATGGCCCATTCACCGATCTCTGG 200
Qy 122 CGGCGGTTGAATATTTGATTCCTTTATCGACCGCGTGCCTTACCCGCTTGCCTGA 181
Db 201 AGCTGGTTTGAACATCCTCATCCTGTGTAGACCGGATCCGATATGTGACAGATCTCA 260
Qy 182 AAGAAATCCCTTGAAGTACCCAGAGCTGACATCAGCGGGAATTAACGAATGA 241
Db 261 AGGAAATTTGATCAAGGTGCTGAGCATGCGCTGACTGACTGACAAATGTAATCTCTGC 320
Qy 242 CTGTTGACGCAATCTATTTCAGATACCGATCCAAACTCGCTTACATCGGTTGCA 301
Db 321 AAATGATGAGAGTCTTTACCTGCGCATGAGACCTTGAAGGCAAGCTACGGTGG 380
Qy 302 GCAACTATATGAGCAATTAACCAAGCTTGCCCAAGAGCGCTGCTTCCGTTATCGGCG 361
Db 381 AGGACCTGAGTAGTCCGTCACCCAGCTAGCTCAAAACCATGATGATGAGAGCTCGCA 440
Qy 362 GTATGAGTTGAGCAAAACGTTTGAAGACGCAAGAAATCAACATGACGCTGCTCCG 421
Db 441 AACTCTCTGGAAGAAAGCTTCCGGAACGGAGTCTTGAAGCCAGCATGTGTGATG 500
Qy 422 CCTCGATGAAGCGCGGCGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATT 481
Db 501 CCATCAACCAAGCTGCTGACGCTGGGATTCGCTGCTCCGTTATGAGATCAAGATA 560
Qy 482 TGGTTCCGCGCAAGAAATCTTCCGCAATGCAAGGCAAAATTAACCGCGAAGCGGAAA 541
Db 561 TCCATGTGCCAACC CGGGTGAAGAGTCTATGAGATGCAAGTGAAGGCGGCGGA 620
Qy 542 AACGCGCCGTAATTGCGGAATCCGAAGCCGTAAATGAAACAAATCAACTTGGCAAGT 601
Db 621 AACGGGCAAGATCTGAGATCTGA-----GG 647
Qy 602 GTCAAGCGTGAAGCCGAATCCAAATCCGAAGGCGAGGCTCAGGCTGCGTCAATCGT 661
Db 648 GAGCCGAGAGTCCGCGCATCAATGTGCAAGAGGAGGAAACAGGCGCAATCTGGCCT 707
Qy 662 CCAATGCCGGAAGAAATGCGCGCATCAACCGCGCAAGGCGAAGCGAAATCCCTGCGCC 721
Db 708 CCGAAGCAAGAAAGGCTGAACAGATTAATCAGGAGCAGAGAGAGGCGAGTCTGG 767
Qy 722 TTGTTGCCGAAGCAATGCGGAAGCCATCCGTAATTTGCGCGCCCTTCAAAACCAAG 781
Db 768 CGAAGCGCAAGGCTTAAGCTGAAGCTTAATTCGATTCCTGCGTGAAGCTTACCAACATA 827
Qy 782 GCGGGCGGAGTCCGCTCAATCTGAAGATGCGGAACAAATGAGAGCGGCTTCAACATC 841
Db 828 ATGAGATGCAAGAGCTTCACTGACTGTGCGGAGAGATATGTGAGGCGCTTCTCCAAAC 887
Qy 842 TTGCGCAAGAAAGCAATACGCTGATTAATGCGCGCATGTTGCGCATGCGGAGCTGGA 901

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Db 888 TGGCCAGAGCTCCACACTATCTACTGCTCCACACCTGCGATGTACACAGATG 947
 QY 902 TTTCTGCGGCATG 915
 Db 948 TGGCTCAGGCCATG 961

RESULT 20
 BX400955 1023 bp mRNA linear EST 29-APR-2004
 LOCUS BX400955 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DK005YE05 5-PRIME, mRNA sequence.
 ACCESSION BX400955
 VERSION BX400955.2 GI:46878596
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1023)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30626315.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr; Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5178.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cda?c=CS0DK005AC03QPIc=5178.r.
 Location/Qualifiers
 1..1023
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK005YE05"
 /cell_line="HELA"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 16.3%; Score 154.4; DB 5; Length 1023;
 Best Local Similarity 49.0%; Pired. No. 1.3e-34; Indels 33; Gaps 1;
 Matches 432; Conservative 13; Mismatches 404;

QY 62 TCATCCCCCAGAGAGTCCAGTGTGCAAGGCTCGGCGCTTTCATCGGCCCTGA 121
 Db 141 TGTGCGGAGAGAGGCTGTGAGGAGATGGCGCATTCACCGGATCTCTG 200
 QY 122 CGGCGGTTGAATATTTGATTCCTTTATCGACCGGCTGACCGCATTCCTGA 181
 Db 201 AGCGTGTGTAACATCTCATCTCTGTGTAGACCGGATTCGATGTGCGAGATCTCA 260
 QY 182 AAGAAATCCCTTGAAGAGTACCGAGGAGTGTGATCGAGGAGTAATAGCAATTA 241
 Db 261 AGGAAATGTGTCACACGCTGAGAGAGTGGCTGTGATCTTGACAAATGTAACTGCG 320
 QY 242 CTGTGACGCGCATCATCTATTTTCAAGTAAACGATCCCAATCGGCTCATAGCGTTCA 301
 Db 321 AATGATGAGAGTCTTTACCTGCGCATATGACCTTAAAGGCAAGTACGAGTGG 380
 QY 302 GCAACTACATTAATGCAATTACCCAGCTTGCACAAAGACGCTGCTTATCGGGC 361

Db 361 AGGACCTGAGATGCCGTGACCCGAGTACGCTCAAAACAACATGATCAAGCTCGGCA 440
 QY 362 GTATGAGTGGACAAAACGTTTGAAGAACCGGACGAAATCAACGTAACCGTCTCG 421
 Db 441 AACTCTCTGTGACAAATCTTCCGGGAAAGGAGATCCCTGAATCCAGCATTTGGATG 500
 QY 422 CCCGTGATGAAGCGCGCGGCTTGGAGTGTGAAGTCTCTCGTTACGAAATCAAGATT 481
 Db 501 CCATACCAAGCTGTCTACTGCTGGGATATCCGCTGCTCCGTTATGATCAAGATA 560
 QY 482 TGGTTCGCGCGCAAGAAATCTTCCGCGATGACGACGCAAAATTACCGCGAAACGGA 541
 Db 561 TCATATGTCACCCCGGATGAAGAGTGTATGACAGATGACAGGTGAGGACGCGCGGA 620
 QY 542 AACGCGCGGATTTGCGCAATCCGAGAGCCGTAATAATGAAACAAATCAACTTGCAGTG 601
 Db 621 AACGGGCCACAGTTTGAAGTCTGA-----GG 647
 QY 602 GTACAGCTGAAAGCCGAATTCACAAATCCGAAGGAGGCTCAGGCTGCGGTCAATGCGT 661
 Db 648 GGACCCGAGAGTGGCCATCAATGTGCGAGAGGAGAAACAGGCCCCAGATCTGGCT 707
 QY 662 CCAATGCCGAGAAATCCCGCCGATCAACCGCGCAAGCGGAGCGGAATCCCTGCGCC 721
 Db 708 CCGAGCGAAGAAAGGCTGAACAGTAATCAGGAGGAGGAGGCGAGTCACTTCTG 767
 QY 722 TTGTTCCGAGAACCAATGCCAGAGCATTCGTAATTCGCGCGCTTCAACCCAG 781
 Db 768 CGAAGCGCAAGGCTAAACCTGAAGCTATTCGATCTGCTGACCTCTGACACAAATA 827
 QY 782 GGGGGCGGATGCGGTCAATCTGAGATTGGGGAACATAGTAGCGGCTTCAACATC 841
 Db 828 ATGAGATGACAGCACTTCACTGAGCTGTGGCGGACAGATATTCAGCGGTTCTCAAC 887
 QY 842 TTGCCAAAGAAAGCAATACGCTATTATGCCCGCAATGTTGCCGACATTCGAGCTGA 901
 Db 888 TGGCCAGAGGCTCCACACTATCTACTGCTCCACACCTGCGATGTACACAGATG 947

QY 902 TTTCTGCGGCATGAAATTTATCGACAGCAAAACGCCCA 943
 Db 948 KGSITCAAGCCATYGKGTATTATGRCGCCACCAARCCMR 989

RESULT 21
 COS48169 906 bp mRNA linear EST 01-SEP-2004
 LOCUS LYEST5061 Sea lamprey LyEST Petromyzon marinus cDNA, mRNA sequence.
 DEFINITION COS48169
 ACCESSION COS48169.1 GI:51796481
 VERSION EST.
 KEYWORDS Petromyzon marinus (sea lamprey)
 SOURCE Petromyzon marinus
 ORGANISM Petromyzon marinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 Petromyzontiformes; Petromyzontidae; Petromyzon.
 1 (bases 1 to 906)
 Pancer, Z., Meyer, W.E., Klein, J. and Cooper, M.D.
 Prototypic T-cell receptor and CD4-like coreceptor expressed in
 lymphocytes of the agnathan sea lamprey
 Proc. Natl. Acad. Sci. U.S.A. 101, 13273-13278 (2004)
 Contact: Pancer, Zeev
 Division of Developmental and Clinical Immunology
 The University of Alabama at Birmingham
 378 Wallace Tumor Institute, 1530 Third Avenue, South, Birmingham,
 AL 35294-3300
 Tel: 205-975-5812
 Fax: 205-975-7218
 Email: zpancer@uab.edu

FEATURES
 source 1..906
 /organism="Petromyzon marinus"
 /mol_type="mRNA"
 /db_xref="taxon:7757"

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/cell_type="lymphocyte"
/dev_stage="unstimulated larvae"
/clone_id="Scs lamprey LyEST"
/note="Vector: Lambda Zap Express; lymphocyte mRNA ESTs from unstimulated larvae. All are from arrayed colonies from a directionally cloned cDNA library in Lambda Zap Express (Stratagene). All are single pass 5' sequences."

```

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/clone_11b="Sea lamprey LYST"
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/note="Vector: Lambda ZAP Expr
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from a directionally cloned cDNA library in lambda ZAP

ORIGIN

Query Match	16.2%	Score 153.4	DB 7	Length 906
Best Local Similarity	50.8%	Pred. No. 2.4e-34		
Matches 367	Conservative	0	Mismatches 356	Indels 0
			Gaps	0

QY	48	CAAAATCCCTTTGCTGCATCCCCACGAGAAAGTCCAGTTCGCGAAAGGCTCGGCGCTTT	107
Db	166	CACGGCCCTGCTGTTCCTGTCGCCGACAGAGAGCGCTGGAATCATACAGCCGCAATGGACAGATT	225
QY	108	CCATTCGCGCCCTGACGCGCCGGTTTGAATATATTTTGAATTCCTTTATTCGACCGCGTGCCTTA	167
Db	226	CCACCCGGTACTCCGGGCGGGTTTGAATCTTCTGATCCCGAATATTCGACAGAAATTAAGTA	285
QY	168	CCGCCATTCCGCTGAAAGAAATCCCTTTAGAGTACCCGACCCAGGCTCTGATTCACGGCGGA	227
Db	286	CGTCGAGAGCTTGAAGAGAAATAGTCATCGACATTCGCCAGCAGTTCGCATCACCTCTGGA	345
QY	228	TAATACGCAATTGACCTGTTGACGGGATCATCTATTTCCAGTAAACGATCCCAACTCGC	287
Db	346	TAATGTTACATCAACATCGATGAGTGTGTGTTGTACTCCGCAATTATGACACCGCTTAAGGC	405
QY	288	CTCATACGGTTTCGAGCACTACATTTATGCAATTAACCGAGCTTGGCCCAAACGACCTGCG	347
Db	406	GAGCTACGGCGCTCGAGGACCCCGAGTACGCGGTGAACCAAGCTGAGCTCAGACCAACATCGG	465
QY	348	TTCCGTTATCGGCGGTATGAGATTGAGCAAAACGTTTGAAGAAGCCGACGAAATCAACAG	407
Db	466	CTTCGAGCTGGGCAAGATCGCGCTGGAACAGCGTGTTTAAGAGAGAGAGTCTTGAAAGGC	525
QY	408	TACCGTGGTCCCGCCCTCGATGGAAGCCGCGGGCTTAGGGGTGGAAGTCTTCGCTTA	467
Db	526	CACACTTGTGAGGTGATTAATTTAGGGCGGCGGAGGTATGGGGCATTCGTTGCTTCGGCTA	585
QY	468	CGAAATCAAGGATTTGTTTCCGCGCAAGAAATCCTTCGCGCAATGACGACCAAAATTAC	527
Db	586	CGAATCAAGGACATGAGAGCTGCCAACCGCGGTCAAGGAAGCCANTGACAGATGCAGGTGA	645
QY	528	CGCCGAACGCAAAAACGCGCCCGTATTGCGGAATCCGAAAGCCGTAAATTCGAACAAT	587
Db	646	GGCCGAGCGGCGCAAGCAGCGCGTGTGCTCGGAAGTCGAGGCGCAATTCGAGTCCGACAT	705
QY	588	CAACCTTGCCAGTGGTCAAGCGTGAAGCGGAATCCACAATTCGGAAGGCGAGGCTCAGGC	647
Db	706	CACGTGGCCGAGGGCAAGAGCGCTCAGCACTCTCGCTTGAGAGGCTGAAAAGGCGGA	765
QY	648	TGCGGTCAATGCTGTCATGCGCGAAGAAATGCGCCGCATCAACCGCGCCAAAGCGGAAGC	707
Db	766	GCAAGTCAACAGAGAGAGAGGCCAAGCGTCCGCAATGGTGAAGAAAGCCATTCGCAAAAGC	825
QY	708	GGAATCCCTGCGCCTTGTTCGCGAAGCCAAATGCGAGACCATTCGTCAAATTTGCCCGC	767
Db	826	GGAAGCCATCAACGCGGCTGCGAGAGGCCCTCAGCGAGCAAGAACGGCAACATGCGCGCTC	885
QY	768	CCT 770	
Db	886	GCT 888	

RESULT 22	CNS08NXD/c	LOCUS	DEFINITION
	CNS08NXD	947 bp	mbNA linear
			Single read from an extremely of a full-length cDNA clone made from
			Anopheles gambiæ total adult females. 3-PRIME end of clone
			FX0AA30D01 of strain 6-9 of Anopheles gambiæ (African malaria
			mosquito).

ACCESSION	EX020429
VERSION	EX020429.1
KEYWORDS	GI:27569649
SOURCE	HTC.
ORGANISM	Anopheles gambiae (African malaria mosquito)
	Anopheles gambiae
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
	Anophelinae.
REFERENCE	1 (bases 1 to 947)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr
FEATURES	- Web : www.genoscope.cns.fr
source	location/Qualifiers
	1..947

Query Match	16.1%	Score 152.2	DB 3	Length 947
Best Local Similarity	53.9%	Pred. No. 5.6e-34		
Matches 313; Conservative	0	Mismatches 268	Indels 0	Gaps 0

OY	154	GACCGCGTCGCGCTACCGCATTCGCTGTAAGAAATCCCTTTAGACGTACCCGACGCTC	213
Db	947	GACCGCGTGAAGTATGCTGACAGTCTGAAGGAAATCGAATAGACGTGCCGAAACAGTCC	888
OY	214	TGCATCAGCGCGGATATATCGCAATTGACTGTGACGCGATCATTTATTTCCAGTAAC	273
Db	887	GCCATCAAGTCCGACCAAGTAACGCTCAGCATCGACGCTGTGCTGTACTTGCGCATTCCTC	828
OY	274	GATCCCAAACTCGCTCATACGTTTCAGGCACTGATTTATGCGAATTACCGAGTTGCG	333
Db	827	GACCCGTACTCGCGCTCGTACGCTGTGAGAGACCCGAGTTTGCCATACCCAGCTCGCC	768
OY	334	CAAAAGACGCTGCGCTTCGTTATCGGCGGTATGAGATTGAGCAAAACCTTTGAAAGACG	393
Db	767	CAACGACGATGCGCTCCGACGTGGGCAAGATGTACTGACACAGTGTTCGGGAGCGCC	708
OY	394	GACGAATCAACAGTACCGTGTCTCGCCCTCGATGAAGCCGCGGAGCTTTGGGCTGTG	453
Db	707	GAATCGCTCAACATCAGCATGTGTGAGTGCATCAACAAGCGCAGCGAAGCGTGGGCGATC	648
OY	454	AAAGTCTTCGCTTACGAATCAAGATTGTGTTCCGCGCGCAAGAAATCCTTCGCGCATG	513
Db	647	TCTGGCTGCGGTACGAATCCGCGACATCAAGCTCGGAGCGGGGTSCACGAACGATG	588
OY	514	CAGCACAAAATTACCGCGCCGACGCGAATAACGCGCCGCTATTGCGGAATCCGAGGCGGT	573
Db	587	CAGATGCAAGTGTGAGGCGGAGCGCGACGACGCGGCTCGGATCTTGAATCGAGGGTGTTC	528
OY	574	AAAAATCGAACAAATCAACTTGTGCCAGTGTGACGCTGGAAGCGCAATCCAAATCCGAA	633
Db	527	CGGGGCGCGCAATTAACTGTGGCGAGGGTAAAGCAGATGTCGCGCTCTTGCCGAG	468
OY	634	GCGGAGGCTCAGGCTGCGGTCAATGCTGTCAATGCGGAGAAATGCGCCGATCAACGCG	693
Db	467	GCGCAGAAAGCAGGAGAGATCAATCGCGCGAATGGTGTGAGGGCGGCGCGCATATGGCGCTG	408
OY	694	GCCAAAGCGAAGCGGAAATCCCTGCGCTTGTGCCGAAGC	734
Db	407	GCCGATGCGGTGCGAAAAGTCTGAATAATGTGTGCCGAATC	367

RESULT 23	
CN124718	
LOCUS	
CN124718	847 bp
	mRNA
	linear
	EST 01-APR-2000

DEFINITION RHOH1_6_B03.g1_A002 Acid- and alkaline-treated roots Sorghum
 bicolor cDNA clone RHOH1_6_B03_A002 5', mRNA sequence.
 ACCESSION CN124718
 VERSION CN124718.1 GI:45948467
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 847)
 Cordonnier-Pratt M.-M., Suzuki Y., Sugano S., Klein R., Liang C.,
 Sun F., Sullivan R., Lim S., Eastman A. and Pratt L.H.
 An EST database from Sorghum: acid- and alkaline-treated roots
 Unpublished (2003)
 Other ESTs: RHOH1_6_B03.b1_A002
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yuraka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science; plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).
 Location/Qualifiers
 1..847
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 /mol_type="mRNA"
 /db_xref="taxon:4558"
 /db_xref="Btx623"
 /clone="RHOH1_6_B03_A002"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_1fb="Acid- and alkaline-treated roots"
 /note="Organ: Root; Vector: pME18S-Fl3; Site_1: XhoI;
 Site_2: XhoI; The library was prepared from polyA+ RNA
 from 8-day-old roots harvested from Btx623 sorghum
 seedlings grown in hydroponic culture. HCl was added to a
 pH of 3.0 to some seedlings, KOH to a pH of 9.0 for
 others. Roots were harvested 3, 12 and 27 hr after
 addition and pooled for RNA preparation. Double-stranded
 cDNA was cloned unidirectionally into different DraIII
 sites of the pME18S-Fl3 vector (5-prime DraIII site is
 CACTGTGT, 3-prime DraIII site is CACCATGTG). XhoI excises
 the cDNA insert."

ORIGIN

Query Match 16.0%; Score 151.4; DB 7; Length 847;
 Best Local Similarity 55.4%; Pred. No. 9.4e-34;
 Matches 293; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

60 CCGTATCCCGCCAGAGAGTCCAGTTCGAGAAAGCTCGGCGTTTCATCGCGCCCT 119
 DB 297 CATAGTCCCGAGAAAGGCTTTCGTCATCGAGAGTTCGGAAGTATCTCAAGACGCT 356
 QY 120 GACGCGCGGTTGAATATTTGATTCCTTTATCGACCGCGTGCCTACCGCCATTCGCT 179
 DB 357 CGGCTCGGGTTCCACTCTGTATCCCGCGCGGACCGATCGCTTAGTGACCTCGCT 416
 QY 180 GAAAGAAATCCCTTGAAGCTACCGACGAGTGTGATACCGCGGATTAATCGCAATT 239
 DB 417 CAAGAGAGAGACCATCCCGTCCCGACCAAGCGCATCAACAGAGCAACCTCAACAT 476
 QY 240 GACTGTGACGAGATCATTAATTCACAGTAACGATCCCAACTCGCCCTCATACGAGTTC 299
 DB 477 ACAGATGACAGGCTCATATGATCAAGATCAAGACCCCTTACTTCTTATGGTGT 536

QY 300 GAGCACTACATTATGGCAATTACCCAGCTTGCCCAACGACGCTGCGTTATCCG 359
 DB 537 GAGAGATCAATCTATGCTGTCTTACACCTTGACAAACCAACATGAGAAGTGAATTGG 596
 QY 360 GCGTATGAGTTGGACAAACGTTTGAAGAACGCGACAAATCAACAGTACCGTCTCTC 419
 DB 597 GAAGATACCTTGAACAAAGACTTTTGAAGAGAGATGATCAATTAATGAGAAATTTGAG 656
 QY 420 GCGCTCATGAAGCCCGCGGCTTTGGGGTGTGAAGTCTCTCGTTACGAAATCAAGA 479
 DB 657 TGCCATCAATGAAAGCAGCACAGATGTGGGCTTGAGTATCCGCTATGAGATTAGGA 716
 QY 480 TTTGGTTCGCGCGCAAGAAATCCTTGCGCAATGACGACCAAAATTACCGCGAAGCGA 539
 DB 717 CATTACTCTCTCAATAGGATTAAGCAGGCTTATGAGATGAGGCTGAAGCAAGAAAGAG 776
 QY 540 AAAAGCGCCCGTATTCGGAATCCGAAGCGCGTAAATCGAAACAAATC 588
 DB 777 AAAAGCGCCCGAAATCTTGATCGGAAGGGAAGAAACAGCCCAATC 825

RESULT 24
 CNS09K89
 LOCUS
 DEFINITION Single read from an extremity of a full-length cDNA clone made from
 Anopheles gambiae total adult females. 5-PRIME end of clone
 FK0AAC33CB04 of strain 6-9 of Anopheles gambiae (African malaria
 mosquito).
 ACCESSION BX062293
 VERSION BX062293.1 GI:27635574
 KEYWORDS HTC
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anophelinae.
 1 (bases 1 to 897)
 Reference
 AUTHORS Direct Submission
 TITLE Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 JOURNAL - Web : www.genoscope.cns.fr
 Location/Qualifiers
 1..897
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="6-9"
 /db_xref="taxon:7165"
 /clone="FK0AAC33CB04"
 /plasmid="pME18S-Fl"
 /note="end : 5-PRIME"

ORIGIN

Query Match 15.8%; Score 149.4; DB 3; Length 897;
 Best Local Similarity 53.9%; Pred. No. 3.8e-33;
 Matches 349; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

65 TCCCCAGCAGGAAGTCCAGTTCGAAAGGCTCGGCGTTTCATCGCGCTTGACGG 124
 DB 252 TGCCCAAGAAAGGATCGTGAAGGATGGGCAAAATTTACCGCATCTCGAGC 311
 QY 125 CCGGTTGAATATTTGATTCCTTTATCGACCGCGTGCCTTACCGCCATTCGCTGAAG 184
 DB 312 CCGGCTGAAGCTCTGTCGCGCGTGTGAACCGGCTGAAGTACGAGCTGAAG 371
 QY 185 AATTCCTTAAAGCAAGCAGCAGGCTGATCAAGCGGATTAATGCAATGACG 244
 DB 372 AATTCGAATAGACGCGGAAACAGTCCGCAATACGTCGCAACGTAAGCTCAGCA 431
 QY 245 TTGACGCGATCATTAATTCGAAAGTACCGATCCCAACTCGCCTCATACGAGTTCGAGCA 304
 DB 432 TCGAGGCTGTGCTGATCTGCGGATTCGACCCGTAACCTCGGCTGTGAGTGTGAGAG 491

Oy	305	ACTACATTATGAGCAATTTCACAGCTTGCACAAAGACGCTGGTTCCGTTATCGGGCGTA	364
Db	492	ACCAGGAGTTTGCCATTCACCCAGCTGCCCAAGCAAGATGCGCTCCAGCTGGGCAAGA	551
Oy	365	TGAGATTGGAACAAACGTTTGAGAGACGACGAAATCAACAGTACCGTGTCTTCGGCCC	424
Db	552	TGTCACTGGACAAAGGTGTTCGGGAGCGCGAATGCTCAACATCGATCGTGGAGTGA	611
Oy	425	TCGATGAAGCCGCCGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGAATTGG	484
Db	612	TC-AACAAAGGCGAGCGAAGGAGGAGCATCTCTGCTCGGTACAAATTCGCGCATCA	670
Oy	485	TTCCGCGCCAAAGAAATCCCTGCGCATATGACAGGCACAATTAACGCCGCAAGCAAAAC	544
Db	671	AGCTGCCAGCGCGGTGACAGAGGATGTCAGATGCAAGTGAAGCGGACGCG-CAAGC	729
Oy	545	GCGCCCGTATTGCGCAATTCGAAAGGCGGTAAATCGAAACAATCAACTTGCCAGTGTCTC	604
Db	720	GGGCGCGATCCTCGAGTCGAGGAGGTGTCCGGCGCGCGACATTAACTGCGCCGAGGGTA	789
Oy	605	AGCGTGAAGCGGAATTCACAAATCCGAAAGGAGGAGGCTCAGGCTCGGTCAATGTGTCA	664
Db	790	AGCGCAATTCGCGCATCTTGCTTCGAGGCGCAAGACGAGAGATCAATCGGCGCA	849
Oy	665	ATGCCGAGAAATCGCCCGCATCAACCCGCCCAAGCGAAGCGGAA	711
Db	850	ATGCTGAAGCGCGCCGCATCATGTGGGCTGTGGCCGATGCCGCTGCCGAA	896
RESULT 25			
CB620196/c			
LOCUS	CB620196	657 bp	mRNA linear EST 08-APR-2003
DEFINITION	OSIIa05D17.r OSIIa Oryza sativa (indica cultivar-group) cDNA		
ACCESSION	CB620196		
VERSION	CB620196.1	GI:29615183	
KEYWORDS	EST.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group)		
REFERENCE	Oryza sativa (indica cultivar-group)		
AUTHORS	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
TITLE	1 (bases 1 to 657)		
JOURNAL	Jantaasriyarex,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.		
COMMENT	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe oryzae		
UNPUBLISHED	(2003)		
CONTACT	Arizona Genomics Institute		
UNIVERSITY	University of Arizona		
ADDRESS	Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA		
TELEPHONE	Tel: 520 626 3967		
FAX	Fax: 520 621 9288		
EMAIL	Email: http://genome.arizona.edu		
PCR	PCR Primers		
FORWARD	gta aac cga cgg cca gtc		
BACKWARD	gga aac agc tat gac cat g		
PLATE	05 row: D column: 17		
SEQ	Seq primer: gga aac agc tat gac cat g.		
LOCATION	Location/Qualifiers		
1..657			
/organism	=Oryza sativa (indica cultivar-group)"		
/mol_type	=mRNA"		
/cultivar	=IR36"		
/db_xref	=taxon:39946"		
/clone	=OSIIa05D17"		
/tissue	=leaf"		
/dev_stage	=u3 week"		
/lab_host	=DH10B"		
/clone_lib	=OSIIa"		
FEATURES			
SOURCE			

ORIGIN	Query Match	15.7%	Score 148.8	DB 6	Length 657	
	Beat Local Similarity	54.3%	Pred. No. 5.2e-33			
	Matches 300	Conservative 0	Mismatches 252	Indels 0	Gaps 0	
QY	60	CGTATCCCCAGAGAGAGTCCACGCTTGTGCGAAAGGCTGGGGGTTCCATCGCGCCCT	119			
DB	552	CATGTCGCCGAGAGAGAGAGGCTTCGCTGGAGACGGTTCGGCAAGTCAAGACGCT	493			
QY	120	GAGCGCGGGTTGAATATTTTGAATTCCTTATATGACCGCGTGCCTACCGCCATTGCT	179			
DB	492	CGGCTCGGGATTCACGTCGCTGTCGCCCTTCGTGACCGCATCGCTTACGTCACCTGCT	433			
QY	180	GAAGAATATCCCTTTGAGCGTACCCAGCCAGGTCGTGATCAGCGCGCATATATGCAATT	239			
DB	432	CAAGAGAGAGGCCATCCCATCCCGACAGTCGCGCATCAGCAAGCAACGCTCCAT	373			
QY	240	GACTGTGACGGCATCATCTATTTCGAAAGTACCGATCCAAATCGCTTCATACGTTCC	299			
DB	372	CCAGATGACGCGCGCTCCTCTACGTCAGATGTTGTGATCCCTACCTTCCTTATGCTGT	313			
QY	300	GAGCACTCACTTATGCGAATTACCCAGCTTGCCCAACGACGCTGGCTCCGTTATCGG	359			
DB	312	GGAGATTCATATTTTGTGATCATACAGCTTGCCCAACATCTATGAGAAAGTAGCTTGG	253			
QY	420	CGCCCTCGATGTAAGCCCGCGGGCTTGGGGTGTAAAGTCTCTCGTTACGAAATTCAGGA	479			
DB	192	GTCATTAATGAGGCTCAACTGATGTTGGGACGTGAATGCTTACGTTATGATGATCAGGA	133			
QY	480	TTTGGTTCGCGCGAAGAAATCCTTCGCGCAATGCAGACCAATTTACCGCGAAGCGGA	539			
DB	132	TATATCTCCGACAGTGTGTGTTAAGTGGCTATGAGATGCACAGACAGAAAGAGA	73			
QY	540	AAACGCGCCCGTATTCGCCGATCCGAAGGCCGTAAATCGAACAAATTCACCTTGGCAG	599			
DB	72	AAACGCTGCCAAATCCTTGATCAGAAAGTGTATTTGGATCATGTCAAAGGCGGAAA	13			
QY	600	TGTCAGCGTGA	611			
DB	12	GGTGAAGGCTGA	1			
RESULT 26	BM345666	623 bp	mRNA	linear	EST 23-JAN-2002	
LOCUS	rf66e08.y1	Globodera rostockiensis J2 pcdN11	Smant v1	Globodera rostockiensis	cgma 5'	similar to TR:Q9XVP9 Q9XVP9 F30A10.5 PROTEIN.
DEFINITION	[1] : mRNA sequence.					
ACCESSION	BM345666					
VERSION	BM345666.1	GI:18082581				
KEYWORDS	EST.					
SOURCE	Globodera rostockiensis					
ORANISM	Globodera rostockiensis					
REFERENCE	1 (bases 1 to 623)					
AUTHORS	McCarteer,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,					
	McCarteer,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,					
	Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,					
	Bowers,Y., Gibbons,M., Rifter,E., Bennett,J., Franklin,C.,					
	Teagarden,Ivill,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,					
	Underwood,K., Steptoe,M., Allen,M., Peterson,B., Swaller,T.,					
	Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,					
	McCamn,R., Waterson,R. and Wilson,R.					
	The Washington Univ. Nematode EST Project, 1999					
TITLE	Unpublished (1999)					
JOURNAL						
COMMENT	Contact: McCarteer JP					

The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 The library was contributed by Dr. Geert Smant of the Laboratory of
 Nematology at Wageningen University, Wageningen,
 Netherlands (geert.sman@wur.nl). DNA Sequencing by:
 Washington University Genome Sequencing Center
 Seq primer: -40RP from Gibco
 High quality sequence stop: 481.

FEATURES

SOURCE

1. 623
 /organism="Globodera rostochiensis"
 /mol_type="mRNA"
 /db_xref="taxon:31243"
 /dev_stage="J2"
 /lab_host="DH10B"
 /clone_lib="Globodera rostochiensis U2 pCDNAT1 Smant v1"
 /note="Vector: pCDNAT1 (Invitrogen); Site 1: BstXI;
 Site 2: EcoRI; The library was donated for sequencing by
 Geert Smant from Wageningen University, Laboratory of
 Nematology, The Netherlands."

ORIGIN

Query Match 15.5%; Score 146.6; DB 4; Length 623;
 Best Local Similarity 53.6%; Pred. No. 2,3e-32;
 Matches 305; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

65 TCCCCAGAGAGATCCACGCTGTCGAAAGGCTGGGCTTCCATCGCGCCCTGACGG 124
 55 TCCCCAGAGAGATCCACGCTGTCGAAAGGCTGGGCTTCCATCGCGCCCTGACGG 114
 125 CCGGTTGAATATTTGATTCCCTTATGACCGCGCTGCTACGCGCATTCGCTGAAG 184
 115 CCGGATGACATTTGTGGACCGCTTCATGAGTATCGGATTCAGCATCTGTGAAAG 174
 185 AATCCCTTTAGACGATCCAGCCAGCTGTCATCACGCGCATATATGCAATGATG 244
 175 AGATGTCATGAAATCCCTCAAGAGAGCATGCAAGAGCAATGTCATGATGAT 234
 245 TTGACGGCATCATCTATTTCGAAATGACGATCCCAACTCGCTCTATCGGTGAGA 304
 235 TGGATGCCATCTTATATGTGCAAGTGTGACCCGTCACAGGCTTCTTACGAGGCG 294
 305 ACTACATATGCGCATTTACCGAGCTTGGCCCAAGCAAGCGTGGTCCGTTATCGGCG 364
 295 ATCCGGAATATGCGATTTAGCTGACGTGGCAAAACCGTAATGGTGCGGAAGTTG 354
 365 TGGATTTGACAAAAGTTTGAAGACGCGAGCAAAATCAAGTACCGTCTCTCCGCC 424
 355 TGAATTTGATTAACGCTTTCACAGAGCGGCAACTTAACATGGAATTTGTTGAAG 414
 425 TCGATGAAGCGCGCGGGGCTTGGGCTGTGAAGTCTCTCGTTACGAATTCAGAT 484
 415 TCAAGGAATCCGCTTCAACATGGGGCTTATTTGTTCTTACGAATTTCCGACAT 474
 485 TTCCGCGCGCAAAATCTTTCGCGCATGACAGCAAAATTAACCGCGCAAGCGGA 544
 475 ACATGCGACCGGAATTCAGCGGTGCATGAAATGCAAGTGAAGGCGAGCGGA 534
 545 GGGCCGCTATGCGCAATCCGAAGCGCGTAAATCGAACAATCAACTTTCGCGCAT 604
 535 GTCCGCGCAATTTTGAATCAGAGGCGATCTCGAAGCGGAAAGAACCGTGGAG 594
 605 AGCGTGAAGCCGAATTCGAATCCGAA 633
 595 AAAAGCAGGCTGCAATTTGCGCTCGAA 623

RESULT 27
 AL722012

LOCUS AL722012 712 bp mRNA linear EST 18-APR-2002
 DEFINITION AL722012 Danio rerio embryonic inner ear subtracted cDNA Danio
 rerio cDNA clone BNOA0572A10 3', mRNA sequence.
 ACCESSION AL722012
 VERSION AL722012.1 GI:20186616
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

REFERENCE

1 (bases 1 to 712)
 Coimbra, R., Weil, D., Brothier, P., Blanchard, S., Levi, M.,
 Hardelin, J.P., Weisenbach, J. and Petit, C.
 A subtracted cDNA library from the zebrafish (Danio rerio)

TITLE

embryonic inner ear

JOURNAL

Unpublished (2002)
 Contact: Genoscope
 Genoscope - Centre National de Séquençage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

SOURCE

1. 712
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="BNOA0572A10"
 /tissue_type="inner ear"
 /dev_stage="embryonic"
 /clone_lib="Danio rerio embryonic inner ear subtracted
 cDNA"
 /note="subtracted cDNA library"

ORIGIN

Query Match 15.3%; Score 145.4; DB 1; Length 712;
 Best Local Similarity 54.3%; Pred. No. 5,6e-32;
 Matches 287; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

140 TGAATCCCTTATTCAGACCGCGCTGCTACCGCATTCGCTGAAGAAATCCCTTAGAG 199
 3 TCATCCGATCTTTCACCGCGCTGCTGCAAGTGAATGATGAGCAGGTGCTGACA 62
 200 TACCGAGCGGCTGTCATGACGCGCATTAATACCAATGCAATGCACTGTCGCGCAT 259
 63 TTCCGGGCGAGAAATCATCAACAGACATGCAATGATCGCGGTCATGCGCTGCT 122
 260 ATTTCGAATGACGATCCCAACTGCTCTATACGTTGAGCAACTATATGCGAA 319
 123 TCTTCAGGTGCTGATGCGCGCGCGCTTATGAGGTGACGCACTTATCTTGCGA 182
 320 TTACCGAGCTTCCCAAGACGCTGCTGCTTATGAGGCTATGAGTTGACAA 379
 183 TCATGACCTGACGACACCACTCAANAACTGATGAGGCTGATGACCTGACGAA 242
 380 GCTTTGAAGAGCGACGCAATCAACAGTACCGTCTCCGCTCGATGAAGCGCG 439
 243 CCGCTTGAAGGCGACATATCAACGCGGCTGCTGCTGCTGATGAGCAAGCACT 302
 440 GGGCTTGGGGTGAAGTCTCGTTACGAATCAAGATTTGTTCCGCGCAAGAA 499
 303 CCGCTTGGGGTGAAGTCAACCGGCTGATCAAGGACATCCGCGCGCGCA 362
 500 TCTTGGCGCAATGACGCAAAATTAACCGCGCAAGCGCAAAAGCGCGCTAT 559
 363 TTTCGAACCGATGCGCGCGCATGAGGCGCAAGGCGCAAAAGCGCGCAACT 422
 560 AATCGAAGCGGCTAAATCGAACAATCAACTGCTGATGAGTCAAGCGGAA 619
 423 AGCGCAAGGCAATGCGCGCTTCNAAATCTCTGCGCGCAAGGCTGAAAGCGG 482
 620 TCAACAATCCGAAGCGGCTGAGGCTGAGGCTGATGCGTCAATGCG 668
 483 TCTGTGAGGCGCAGAGCGCGCGCGGCGCTTTCGCGACCCNAN 531

RESULT 28
CNS0909Q
LOCUS
DEFINITION
CNS0909Q 906 bp mRNA linear HTC 08-JAN-2003
Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 5-PRIME end of clone
FK0A067AC05 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
BX070122
ACCESSION
BX070122.1 GI:27643403
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 906)
Genoscope.
Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1. .906
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0A067AC05"
/plasmid="PM8185-FL"
/note="end : 5-PRIME"
ORIGIN
Query Match 15.3%; Score 145; DB 3; Length 906;
Best Local Similarity 54.5%; Pred. No. 7.9e-32;
Matches 332; Conservative 0; Mismatches 275; Indels 2; Gaps 2;
QY 65 TCCCCAGCAGAGTCCACGTTGTCGAAAGCTCGCGGCTTCCATCGCCCGCTGAGCG 124
DB 254 TCCCCAGCAGAGTCCACGTTGTCGAAAGCTCGCGGCTTCCATCGCCCGCTGAGCG 313
QY 125 CCGGTTGAATATTTTGAATTCCTTTATCGACCGCGTGCCTACCGCCATTG-CTGAAA 183
DB 314 CCGGCTGAACGTCCTGCTGCGCGGTGATGACCGGGTGAAGTACGTGACGAGGTCTGAA 373
QY 184 GAAATCCTTTAGACGTAACCAAGCGAGTCTGCATCAGCCGCGATTAAGCAATTGACT 243
DB 374 GAAATCGCAATAGACGTGCCAACAAGTCCGCATCAGTCCGACAAAGTAAAGCTCAGC 433
QY 244 GTTACGCGCATCATCTATTTCGAAGTACCGATCCAAACTCGCTCATAGGTTTCAGC 303
DB 434 ATCGAGGTGTGCTGTACCTGCGCATTTCCAGCCGTAACCTGCGTGTGATGAGTGA 493
QY 304 AACTACATTATGGAATTAACCAAGCTTGCCCAAGCAAGCTGCGTTCCGTTATCGGGCGT 363
DB 494 GACCCGAGTTTGCATCAACCAAGTGCAGCAAGATGCGGTCCGAGCTGGGCAAG 553
QY 364 ATGAGTTGGAACAAAGCTTTGAAGAGCGCAAGCAATCAACGTAACGTTCTCCGCC 423
DB 554 ATGCACTGGAACAAGTGTTCGGGAGCGCGAATCGTCAACATCAGATGTTGAGTGC 613
QY 424 CTCGATGAAGCGCGCGGGCTTGGGGTGTGAAGTCCCTCGTTACGAATCAAGGATTTC 483
DB 614 ATCAACAAGGAGAGGAGGGGGGAGTCTTCCTGCTGCGGTACGAATTCGGGACATC 673
QY 484 GTTCGCGCAAGAAATCTTCGCGCAATGACAGGCAAAATTAACGCGCAAGGAGAAA 543
DB 674 AAGTCGCGAGACCGGGTGCAGAGAGCATGACAGTGCAGAGCGGAGCGGAGCAAG 733
QY 544 CGCGCCGATTTGCGGAATCCGAAGCGGTAAATTCGAACAATCAACCTTTCGACAGTGT 603
DB 734 GGGCGCGG-ATCTCTGAGTCCGAGGGTGTCCGGCGCGGCAATTAAGTGGCGAGGGT 792

RESULT 29
CD905963
LOCUS
DEFINITION
CD905963 780 bp mRNA linear EST 14-JUL-2003
G468.10324F010809 G468 Triticum aestivum cDNA clone G468103H24,
mRNA sequence.
CD905963
ACCESSION
CD905963.1 GI:32680292
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 780)
Genopiante.
Genopiante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (<http://www.genopiante.com>
and <http://genopiante-info.infobiogen.fr>).
Location/Qualifiers
1. .780
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/mol_type="mRNA"
/cullivar="rectal"
/db_xref="taxon:4565"
/clone="G468103H24"
/issue_type="grain (468 degrees per day after
pollination)"
/clone_11b="G468"
ORIGIN
Query Match 15.3%; Score 144.6; DB 6; Length 780;
Best Local Similarity 53.2%; Pred. No. 9.9e-32;
Matches 306; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
QY 60 CGTATCCCCCAGAGAGATCCACGTTGTCGAAAGCTCGGGGCTTCCATCGCGCCT 119
DB 55 CATGTGCCGAGAAAGAGCTTGTGATGAGCGCTTGGCAAGTACCTCAAGAGCT 114
QY 120 GACGCGGATTGATATTTTGAATTCCTTTATGACCGGCGTGCCTACCGCATTCGT 179
DB 115 GCACTCCGGATCCAGGATCTGCCCCCTCGTGAACCGCATGCCATCGACATCTCT 174
QY 180 GAAAGAAATCCCTTTAAGACGTACCGACCAAGTCTGATCATCAGCGCGATTAATGCAATT 239
DB 175 CAAGAGAAAGACATCCCAATCCCGACAGTCCGATATCAACAAGATTAACGATCAT 234
QY 240 GACTGTGAGGATCATCTATTTCGAAGTACCGATCCCAACTCGCCCTCATACGTTTC 299
DB 235 CCAGATGACGGGCTCTCTTACGCAAGATTGTTATCCCTTACGCTTCATATGCGT 294
QY 300 GAGCAATCAATTATGCAATTAACCGAGCTTGCCCAAGCAAGCGTGCCTCCGTTATCG 359
DB 295 GGAATATCCATTTTTCAGTCACTTTCAGTTCGCGAACAATATGAGTGAAGTGGCTGG 354
QY 360 GCGATGAGATTGACAAAAGTTTGAAGAACGCAAGAAATCAACGATACCGTGTCTC 419

Db 355 AAAGTAACCTTGCACAGACTTTTGAAGAGAGACACATTGATGAGAGATGCTGAG 414
 Qy 420 CGCCCTCATGAAGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGA 479
 Db 415 GTCCATAATGAGGCTTGACAGACTGGGGCTTGAAGTGTCTTCGTTATGATCAGGA 474
 Qy 480 TTTGGTTCCCGCGCAAGAAATCTTCGCGCAATGACGACAAATTAACCGCGCAAGCGCA 539
 Db 475 CATTTCTCTCCACCGGGCGTGAAGATGCTATGAGATGACGACGACGCAAGAGAG 534
 Qy 540 AAAAGCGCGCGGTATTTGCGGAATCCGAAGCGCGTAAATCGAACAATCAACTTCGCGAG 599
 Db 535 AAAGGTGCTCAATTTCTCACTCAGAAAGGGCTATGTTGATTCAGGCAACCGCGCAA 594
 Qy 600 TGTGACGCGTGAAGCGCAATTCACAAATCCGAG 634
 Db 595 GGGTGAAGGCTGAAGCGATCTCTCCAGTCAAG 629
 RESULT 30
 AY408617 1062 bp DNA linear GSS 15-DEC-2003
 LOCUS Mus musculus STOML2 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY408617 GI:39764588
 VERSION AY408617.1 GI:39764588
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS 1 (bases 1 to 1062)
 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
 Adams,M.D. and Cargill,M.
 Interfing nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 TITLE
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1062)
 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gate Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 1..1062
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>1062
 /gene="STOML2"
 /locus_tag="HMC3283"
 ORIGIN
 Query Match 15.3%; Score 144.6; DB 9; Length 1062;
 Best Local Similarity 49.8%; Pred.No.1.1e-31;
 Matches 424; Conservative 0; Mismatches 394; Indels 33; Gaps 1;
 Qy 65 TCCCCAGAGAGAGACGTCGTAAGAGGTCGGGGTTTCCATCGCGCCGACGAG 124
 Db 122 TCCCTCAGAGAGAGGCTGGGTGGTGAAGAGGCGCATTCACCGGATCTGGAAC 181
 Qy 125 CCGGTTGAATATTTTATTCCTTATCGACGCGCTCCCTACCGCATTCGCTGAAG 184
 Db 182 CCGGCTGAAGCTCCCTGATCCCGGTGTGACCGCAATCGGTAATGCGAGAGCTCAAG 241
 Qy 185 AAATCCCTTGAAGCTACCGACGAGTGTGATCAAGCGCGATTAATACGCAATTGACTG 244

Db 242 AAATTGTATCAAGTGCTGAGAGCGCGTAACCTTGACAAATGATACATACAA 301
 Qy 245 TTGACGGCATCATATTATTCAGATACCGAATCCAAACTGCCCTCATACGCTTGACA 304
 Db 302 TAGATGAGTCTTTATCTGCGCATCATGATCTCTTAACAGGCAAGTAACTGTGAAG 361
 Qy 305 ACTACATATATGCAATTATCCAGGCTGCGCAAGAGCGAGCGTTCCTGATTCGGGCGTA 364
 Db 362 ACCGAGATATGCTGTCAACCAAGTATGCTCAGACATATGATACAGCTTGCGCAAC 421
 Qy 365 TGAAGTTGACAAAAGTTTGAAGAACCGACGAATCAAGATACAGTACGCTGCTCGGCC 424
 Db 422 TCTCTCTGACAAAGTTTTCGGAGCGTGAATGCTCCTGAATGCCAAATTTGATGCCA 481
 Qy 425 TCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTTCGTTAGCAATTCAGAGATTGG 484
 Db 482 TCAACCAAGCTGACAGTCTGGGGTATCCGATGCTGCGATACAGATCAAGACATCC 541
 Qy 485 TTCCGCGCCAGAAATCTTTCGCGCATATGACGACCAATTAACGCGGACGCAAAAC 544
 Db 542 ATGTGCCACTCGAGTGAAGAGTCTATGCAAGTACAGTACAGGCAAGCGCGCAAGC 601
 Qy 545 GCGCCGTAATTCGCAATCCGAAGGCGTAAATGCAAAATCAACCTTGCACTGTC 604
 Db 602 GGGCCACAGTCTTAGAGTCCGA -----GGGA 628
 Qy 605 AGCGTGAAGCGGAATTCACAAATCCGAAGCGGAGCTTCAGGCTGCGTCAATGCTCCA 664
 Db 629 CACGAGAGTCAAGCTATTAATGTGCAAGAGGGAAGAAACAGGCCAGATTCCTGCGCTCG 688
 Qy 665 ATGCGGAGAAATGCGCCGCAATCAACCGCGCAAGGGAAGCGGAATCCCTGCGCCTTG 724
 Db 689 AAGCGAAAGAGCTGAACAGATTAATCAAGCGGCGGAGAAAGCACTGAGTCTTGCGCA 748
 Qy 725 TTGCGGAAGCCATCCGAAGGCTGCTCAATTTGCCGCGCTTCAAAACCAAGGCG 784
 Db 749 AGGCCAAGGCTTAAGCCGAAGGATTCGAATTTCTGCGGCTGCTGACTCAACATAAG 808
 Qy 785 GGGCGGATGCGGTCAATGTGAAGATTCGGAACATTAAGCGCGCTTCAACATCTTG 844
 Db 809 GAGATGACGACAGCTTCGCTACTGTGGCTGAGCAGTATGTCAAGCATTTCTCAACTGG 868
 Qy 845 CCAAGAAAGCATACGCTGATTAATGCGCCCAATGTTGCCGACATTCGCAAGCTGATTT 904
 Db 869 CCAAGGATTCCAACAGGTCTACTGCTCCATTCACAGCGACGATGATGTGG 928
 Qy 905 CTGCGCGCATG 915
 Db 929 CTCAGGCGCATG 939
 RESULT 31
 AK002793 1536 bp mRNA linear HTC 03-APR-2004
 LOCUS Mus musculus adult male kidney cDNA, RIKEN full-length enriched
 DEFINITION library, clone:0610038f01 Product:hypothetical protein, full insert
 sequence.
 ACCESSION AK002793
 VERSION AK002793.1 GI:12833037
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS 1
 Carrinci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 Carrinci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

QY 725 TTGCGAAGCCGAGCCGATCCGTAATTCGCGCGCCCTTCAAAACCAAGCG 784
DB 757 AGGCCAAGGCTTAAGCCGAGGATTCGATTCGCGGCTCTGACTCAACTAATG 816
QY 785 GGGCGGATGCGGTAATCTGAAGATTGGCGAACAATAGTAGCCGCTTCAACAATCTTG 844
DB 817 GAGATGACGACGCTTCGCTCACTGTGCTGAGACATATGTGAGCCATTTCTCAAACTGG 876
QY 845 CCAAGAAAGCAATAGCTGATTATGCGCGCAATGTTGCGACATCGGACGCTGATT 904
DB 877 CCAAGGATTCGAACAGAGTACTGCGCTCAATCCGAGCAGCTCAGAGTATGTTGG 936
QY 905 CTGCGCGCATG 915
DB 937 CTCAGGCGCATG 947

RESULT 32
B0579084 705 bp mRNA linear EST 19-JUN-2002
LOCUS WHE2965_C05_F09Z5 wheat dormant embryo cDNA library Triticum
DEFINITION aestivum cDNA clone WHE2965_C05_F09, mRNA sequence.
ACCESSION B0579084
VERSION B0579084.1 GI:21482401
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 705)
Anderson, O.D., Chao, S., Chin, A., Close, T.J., Doherty, L.,
Fenton, R.D., Lazo, G.R., Rausch, C.J., Walker-Simmons, M.K. and
Wilson, C.
The structure and function of the expressed portion of the wheat
genomes - Dormant embryo cDNA library
Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105585773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer
Location/Qualifiers
1..705
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Brevor"
/db_xref="taxon:4565"
/clone="WHE2965_C05_F09"
/tissue_type="Seed embryo"
/dev_stage="Mature seed"
/lab_host="E. coli SOLR"
/note="Vector: lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown to seed
maturity under conditions favoring seed dormancy (L.
Doherty at K. Walker-Simmons lab, Washington State
University, Pullman, WA). Embryos were cut from mature
dormant seed (Doherty). Total RNA was prepared from these
embryos, polyA was purified, a cDNA library was made, and
the cDNA clones were in vivo, excised to give plasmid
plasmids in the 10 Close lab at the University of
California, Riverside (Chin, Fenton). Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

ORIGIN
Query Match 15.0%, Score 142.2, DB 5, Length 705,

Best Local Similarity 53.5%; Pred. No. 5e-31;
Matches 297; Conservative 0; Mismatches 258; Indels 0; Gaps 0;
QY 60 CGTATCCCGACGAGAGATTCACGTTGTGAAGAGCTCGGGCTTTCATCGGCCCT 119
DB 22 CATCGTCCGAGAGAGAGGCTTCGTATGAGGCTTCGCAAGTATTCMAAGCCT 81
QY 120 GACGCGCGTTGAAATATTTGATTCCTTATGACCGCGCTGCTACCGCATTCGT 179
DB 82 CGACTCGGAGATCCAGCGGCTGCTGCTGCTGACGCTACGCTTACGCTCTCT 141
QY 180 GAAAGAAATCCCTTTAGACGTACCCAGCAGTGTGATCA CGCGCATTAATACGCAAT 239
DB 142 CAGAGAGAGAGCAGATCCCATCCCGACAGATCGGCTATGACAGAGATTAAGTGCAT 201
QY 240 GACTGTGACGCGATCATCTATTTTCAGATTAACGATCCCAATCGCTCATACGTTTC 299
DB 202 CCAGATCGACGCGCGCTCTACGTCAAGATTTGATCTTACCTGCTTCATATGCGGT 261
QY 300 GAGCAACTACATTAATGCAATTAACGAGCTTGCCCAACGACGCTGCGTTATCGG 359
DB 262 GAGAGATCCCATTTTTCAGATCATCTTTCGCGACGACATTAATGAAGTGCATTCG 321
QY 360 GCGTATGAGATTGACAAACGTTTGAAGAACGCGACCAATCAACAGTACCGTCTTC 419
DB 322 AAGATTAACCTTTCAGACAAAGCTTTGAGAGAGGACACATTAATGAAGATTTGTAG 381
QY 420 CGCGCTGATGAGAGCGCGCGGCTTGGGCTGTGAAGTCTTCGTTACGAATCAAGGA 479
DB 382 GTCCATTAATGAGGCTTCGACAGACTGCGGCTTGAAGTCTTCGTTATGAATCAAGGA 441
QY 480 TTTGTTTCGCGCGCAAGAAATCTTCGCGCATGAGCGACAAATTAACCGCGAAGCGGA 539
DB 442 CATTTCTCTCCACCGGCGGTGAAGATGATGAGATGACAGAGAGCGAAGAGAG 501
QY 540 AAAAGCGCGCGGATTTGCGGAATCCGAGCGCGTAAATCGAAATCAATCACTTGCAG 599
DB 502 AAGAGGTCTCAAAATTCCTCAGTCAAGAGGGCTATGTTGATCAAGCAACGCGGCA 561
QY 600 TGGTACGCGTGAAGC 614
DB 562 GGTGAGGCTGAAGC 576

RESULT 33
BM423347 1095 bp mRNA linear EST 29-JAN-2002
LOCUS BM423347
DEFINITION AGENCOURT 6402181 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5516467
5', mRNA sequence.
ACCESSION BM423347
VERSION BM423347.1 GI:18391559
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NIH-MGC http://mhc.mci.nih.gov/.
1 (bases 1 to 1095)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contract: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DPF
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1CM2017 row: b column: 20
High quality sequence stop: 503.
Location/Qualifiers
1..1095

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5516467"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming, directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
ORIGIN
Query Match      15.0%; Score 142; DB 4; Length 1095;
Best Local Similarity 50.1%; Pred. No. 6.6e-31;
Matches 410; Conservative 0; Mismatches 375; Indels 33; Gaps 1;

85 GTTGTGAAAGGCTGGGCGTTTCCATGCGCCCGCGGTTGAAATTTGATT 144
   |||||
3  GTGGGAGCGCAATGGGCGCAATCCAGATCCGAGCCTGTTGAACATCCTCATC 62
   |||||
145 CCCTTATGACCGCGCTGCGCCATCCGCTGAAAGAAATCCCTTGAAGCTAAC 204
   |||||
63 CTTGTGTTAGACCGGATCGATATGTCAGAGCTTCAGAGAAATTTGATCACTG 122
   |||||
205 AGCCAGGTCTGCATCACCGCGATTAATAGCAATTAAGTGTGACGCGCATCTATT 264
   |||||
123 GAGAGTGCGGTGTGACTCTGCAATATGTAATCTGCAATATGATGAGTCTTTACTG 182
   |||||
265 CAAGTACCGATCCCAAACTGCTCATACGTTTGACCACTACATTAATGCAATTACC 324
   |||||
183 CGCATCATGAGACCTTTAAGAGCAAGCTACGATGAGAGAGCCTGAGTATGCGTCA 242
   |||||
325 CAGCTTCCCAAGAGCGCTGCTCGTTATCGGCGGTATGAGAGTGAACAAACGTTT 384
   |||||
243 CAGCTAGCTCAAAACATCATGATCAGAGCTCGGCAACTCTCTGTGACAAAGTCTTC 302
   |||||
385 GAAAGAACCGAGCAATTAACGATCCGTCCTTCGCTCGATGAAAGCGCGGAGCT 444
   |||||
303 CGGAGACGGAGATCCTGATATGCGAGATTTGATGTCATCAACAGATGCTGAGTGC 362
   |||||
445 TGGGGTGAAGTCTCTCGTTAGCAATTAAGATTTGGTTCCGCGCAAGAAATCTT 504
   |||||
363 TGGGGTATCCGCTGCTCGTTATGATCAAGATATCCATGTGCCACCCGGGTGAA 422
   |||||
505 CGCGAATGCAAGCAATTAACGCGCAAGCGGAAACGCGCCGATTTGCCAATCC 564
   |||||
423 GAGTTATGCAATGCAATGAGGAGAGCGGCGGAAACGGGCAAGTTCTAGAGTCT 482
   |||||
565 GAAAGCCGTAAATGCAAAATCAACTTGCAGTGTGCTGAGGCGGAAATCCAA 624
   |||||
483 GA-----GGGAGCCCGAGATCGGCGCATCAT 509
   |||||
625 CAATCCGAAGCGAGGCTCAGGCTCGGTCAATGCTCAATCCGAGAAATGCGCCG 684
   |||||
510 GTGGCAAGAGGAAACAAAGCCCAAGATCTGTGGCTCCGAGAGGAAAGGCTGAAAG 569
   |||||
685 ATCAACCGCGCAAGGAGGAGCGGATCCCTGCGCTTGTGGCGGAGCAATGCGGAA 744
   |||||
570 ATTAATTCAGGCGAGGAGAGGCGAGTCAAGTTCTGGGAGAGGCCAAGCTTAAGCTGAA 629
   |||||
745 GCATTCCTCAATTTGCCCGCGCTTCAAAACCAAGGCGGCGGATGCGGTCAATCTG 804
   |||||
630 GCTATTCGAATCTGCTGAGCTCTGACAAACAATAATGAGATGACGAGCTTCACTG 689
   |||||
805 AAGATTCGGAACATACGTAGCGCTTCAACAAATCTTGGCAAGAAAGCAATACGCTG 864
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690 ACTGTGCGGAGAGTATGTCAACGCTTCTCAAACTGGCGCAAGGACTCAACACTATTC 749

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Oy      865 ATTATGCCCGCAATGTTCCGACATCGGACCTGAT 902
Db      750 CTAAGGCTTCACACCTGGGAGATGTCACCAAGATGTT 787

RESULT 34
LOCUS   COS32841
DEFINITION 3530.1.216.1 B02.Y.1 3530 - Full length cDNA library created by
            Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION  COS32841
VERSION    COS32841.1 GI:50337715
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM  Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
           1 (bases 1 to 648)
           Walbot, V.
           Maize ESTs from various cDNA libraries sequenced at Stanford
           University
           Unpublished (1999)
           Contact: Walbot V
           Department of Biological Sciences
           Stanford University
           855 California Ave, Palo Alto, CA 94304, USA
           Tel: 650 723 2227
           Fax: 650 723 8221
           Email: walbot@stanford.edu
           Plate: 3530.1.216.1 row: B
           Location/Qualifiers
             1..648
               /organism="Zea mays"
               /mol_type="mRNA"
               /cultivar="B73"
               /db_xref="taxon:4577"
               /tissue_type="multiple"
               /dev_stage="varies by tissue"
               /lab_host="DH10B"
               /clone_lib="3530 - Full length cDNA library created by
               Invitrogen from multiple tissues"
               /note="Organ: silks, husks, ears, pollen, shoot tips,
               leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
               6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
               Project contracted with Invitrogen to produce a
               normalized, full length library in a pSport vector. This
               is a gateway compatible vector, permitting clone movement
               to new vector backbones for expression in diverse host
               cells using recombination rather than restriction enzymes.
               Details of the vector and sequencing primers are available
               at ZmDB in the EST library description tables. poly(A)+
               mRNA was prepared by Invitrogen, and equimolar amounts of
               RNA from each of the 12 tissue samples were mixed together
               for selection of mRNA with a 5' cap. After syntheses of
               cDNA, a normalization step was conducted against the
               mixture of RNA sources. This step effected a 20X to 80X
               reduction in common transcript types. Tissues prepared: 1.
               just emerging silks; 2. inner husks from ears of sample
               #1; 3. 20 day aleurone; 4. immature tassels, stages from
               1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
               vegetative shoot tips from 15 day old seedlings; all
               leaves with an expanded or partially expanded sheath
               were removed; 8. mature leaf tissue; 9. 0.5 cm long root
               tips from 15 day old seedlings; 10. 10 day whole seed; 11.
               12 day endosperm and embryo; 12. 17 day endosperm and
               embryo. All of the sequenced clones in project 3530 will
               be archived at the University of Arizona along with the
               unigene clones from the Maize Gene Discovery EST
               sequencing projects. Clones can be ordered through the
               ZmDB web site or directly from the University of Arizona
               (http://www.genome.arizona.edu/orders/). High density
               filters containing over 18,000 clones can also be ordered

```

ORIGIN from the University of Arizona."

Query Match 15.0%; Score 141.8; DB 7; Length 648;
Best Local Similarity 54.8%; Pred. No. 6.5e-31;
Matches 281; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

125 CCGGTTTGAATTTTGGATTCCTTATGACCGCGCTTACCGCCATTGGTGAAG 184
6 CCGGTTTCACTCTTGATCCCGCGCTGACCGTATGCTGACGCTGCTCAAG 65
185 AAATCCCTTAGACGACCGACGAGTGTGATCAACGCGCATTAATGCAATTGACTG 244
66 AAGAGACATCTCTTATCTCTTCAACGACGATCAACGACGACGACGACGACGAC 125
245 TTGACGCGATCATCTATTTCCAAAGTAACCGATCCCAACTGCTCTATACGGTTGAGCA 304
126 TTGACGCGATCATCTATTTCCAAAGTAACCGATCCCAACTGCTCTATACGGTTGAGCA 185
305 ACTACATTAATGCAATTACCGACGCTTCCCAACGACGCTGCTGCTTATCGGCGCTA 364
186 ATCCATCTATCTGCTCTCACTCACTTGCACAAACACATGAGAACTGCGGAGAGA 245
365 TGGAGTTGACAAACGTTTGAAGAACGCGAATCAACAGTACCGCTGCTCGGCC 424
246 TTAACCTTAGATTAAGACTTTTGAAGAGAGATGATTAATGAGAAATTTGAGTGC 305
425 TCGATGAAGCCCGCGGCTTGGGCTGTGAAGTCTCTCCGTTACGAAATCAAGATTGG 484
306 TCAATGACGACGACGACGATTTGGGCTGTAAGTATCCGCTATGATGACGACATTA 365
485 TTCGCGCGGACAAATCTTTCGCGCATGCAAGCAAAATTAACCGCGAACCGGAAAAAC 544
366 ATCTCTCAACGAGATTGAGCAGGCTATGAGATGAGGCTGAGGACGAGAAAGAAAAAC 425
545 GCGCCCGTATTCGCCAATTCGGAAGCGCGTAAATCAACAAATCAACCTTGCAGTGTGC 604
426 GCGCTCAATCTTGTAGTGAAGAGAGATGAAGAAAGCGCAAACTCTTGAATGAGAGGA 485
605 AGCGTGAAGCGGAAATCCAAACATCCGAAGCG 637
486 AAAAGACTGCCAGATCTTGAATCTGAAGAG 518

RESULT 35
LOCUS CO010421 967 bp mRNA linear EST 09-JUN-2004
DEFINITION EST798756 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEBH47 5' end, mRNA sequence.

ACCESSION CO010421
VERSION CO010421.1 GI:48517310
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongenaales; mitosporic Ongenaales; Coccidioides.

REFERENCE 1 (bases 1 to 967)
AUTHORS Gardner M.J. and Cole G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST798755
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1..967
/organism="Coccidioides posadasii"
/mol_type="mRNA"

/strain="C735"
/db_xref="taxon:199306"
/clone="CIEBH47"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN
Query Match 14.9%; Score 141.6; DB 7; Length 967;
Best Local Similarity 53.0%; Pred. No. 8.4e-31;
Matches 303; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

65 TCCCCAGACGAGATCCACGTTGTGAAGGCTCGGCGTTTCCATGCGCCCTGACGG 124
309 TTCGACAGACGCGCATGATGTGAGCGGATGGGAAATTTCAACGATTTTGAAC 368
125 CCGGTTTGAATTTTGGATTCCTTATGACCGCGCTTACCGCCATTGGTGAAG 184
369 CCGGATTTGCGATTTCTGATGCGCTTATGACCGGATTTGCTATGTAAGACTTGAAG 428
185 AAATCCCTTAGACGACCGACGAGTGTGATCAACGCGCATTAATGCAATTGACTG 244
429 AAGTGCATGATGATACCAAGTCAAGATCTATACAGCGCATTAACGATGACGCTGAC 488
245 TTGACGCGATCATCTATTTCCAAAGTAACCGATCCCAACTGCTCTATACGGTTGAGCA 304
489 TGGACGAGTGTCTTATTAATGATGTTGAAGCTTGAACAGGCTGATTTGATGATGAAG 548
305 ACTACATTAATGCAATTACCGACGCTTCCCAACGACGCTGCTTATCGGCGCTA 364
549 AGCGGAAATTCGCGATTTCTCAATTTGCGCCACACACATGAGTTGCGAAATTTGCGCAC 608
365 TGGAGTTGACAAACGTTTGAAGAACGCGAATCAACAGTACCGCTGCTCGGCC 424
609 TCACTTAGACACGCTCTTAAAGACGATTAATCTTATGCGATTAATTTCTCAAGCA 668
425 TCGATGAAGCCCGCGGCTTGGGCTGTGAAGTCTCTCCGTTACGAAATCAAGATTGG 484
669 TCAACGAGCGCGCGAGATTTGGGCGTGTATGCTTGTGTTACGAAATTAAGATATCC 728
485 TTCGCGCGGACAAATCTTTCGCGCATGCAAGCAAAATTAACCGCGAACCGGAAAAAC 544
729 ATGCTCTTGAAGAGATTTGGGCTATGATCACTGATCAACGCAAAATTCACAA 788
545 GCGCCCGTATTCGCCAATTCGGAAGCGCGTAAATGAACAAATCAACCTTGCAGTGTGC 604
789 GAGCTGATATTTTGAATCTGAAGTCAAGACGACGACGCAATCAATCGACGAGGATC 848
605 AGCGTGAAGCGGAAATCCAAACATCCGAAGCG 636
849 GGAACATCTCTGATCTTGGCTCCGAAGCC 880

RESULT 36
LOCUS BF263774 814 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CBA0007K04f Hordeum vulgare seedling green leaf EST library,
cDNA clone HV_CBA0007K04f, mRNA sequence.

ACCESSION BF263774
VERSION BF263774.2 GI:13261063
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 814)
Wing, R., Close, T.J., Kleinof, A., Wise, R., Wei, F., Begum, D.,

Best Local Similarity 49.6%; Pred. No. 1,4e-30;
Matches 416; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 48 CAATCTTTTGTCTCATCCCCAGAGAGATCCAGTTGTGAAAGCTCGGCGTT 107
Db 2 CCAAGCGTCCGTTGTCTGTCGAGAGAGAGCTGAGGTGTGAGAGCAATGGCGGATT 61
QY 108 CCATGCGCGCTGAGCGGCGGTTTGAATTTTGAATCCCTTTATGACCGGCTGCTTA 167
Db 62 CCACCGGATCTCGAGCGCTGTTTGAACATCTCTCATCCCTGTGTTAGACCGGATCGAAT 121
QY 168 CCGGCATTCGCTGAAAGAAATCCCTTTAGACGACCCAGAGCTGTCATGACGCGCA 227
Db 122 TGTGACAGTCTCAAGAAATTTGTATCAACGCTGACGAGTGGCTGTGATCTTCA 181
QY 228 TAATACGCAATTTGACTGTGACGCGCATCTATTTCAGATGACCGATCCGAATCCG 287
Db 182 CAATGTAATCTGCAATTTGATGAGTCTTTTACCTGGCATCATGACCTTTACAAAGC 241
QY 288 CTCATACGCTTGAAGCACTACATTTATGCAATTTACCCAGCTTCCCAACGAGCTGCG 347
Db 242 AAGCTACGCGTGTGAGAGACCTGAGTATGCTGTCACCCAGCTAGCTCAAAACAACATGAG 301
QY 348 TTCCGTTATCCGCGCGCATTTGAGATTTGACAAACGTTTGAAGACGAGCAATCAAG 407
Db 302 ATCAAGCTCGGCAAACTCTCTGTGACAAAGTCTTCCGGAACGGGAGTCCCTGATGC 361
QY 408 TACCGTCTCTCGGCTGATGAAAGCCCGCGGCTTGGGCTGTGAAAGCTCCGTTA 467
Db 362 CAGCATTTGATGATGATCATCAACCAAGCTGTGATGCTGAGGATCCGCTGCTCGTTA 421
QY 468 CGAAATCAAGATTTGCTTCCGCGCAAGAAATCTTCCGCGCATGACGACCAATTCAC 527
Db 422 TGAGATCAAGAGATATCATGTGCAACCCGCGGTGAAGAGTATGACATGACAGTGA 481
QY 528 CCGCCGACCGCAAAACCGGCGCGCTTATGCCAAATCCGAAGCGCGTAATGAACAAT 587
Db 482 GGCAGAGCGCGCAAAACGGGCGCAAGTTTGAAGTGA----- 520
QY 588 CAACCTTTCAGATGCTGACGCTGAAGCCGAATTCACAAATCCGAAGCGAGGCTGAGC 647
Db 521 -----GGGACCCGAGAGTCCGCCATCATTTGGCGAAGGGAAGAAAGAGC 568
QY 648 TCCGCTCAATGCGTTCATGCGGAGAAATTCGCGCATCAACCGCGCAAGCGCAAGC 707
Db 569 CCAAGATCTCGGCTCGAAGAGAAAGGCTGAACGATTAATCAGGCGAGAGAGAGG 628
QY 708 GGAATCTCTGCGCTTGTGCGAGAGCAATGCGGCAATTCCTGCAATTTGCCCGC 767
Db 629 CAGTCAATTTCTGCGAGAGCGCAAGGCTTAAGCTGAAGCTTATTCGAATCTGCTGAC 688
QY 768 CCTTCAACCCAGAGCGGCGGAGTGCAGTCAATTTGAAGATTGCGGAACATATCAGTAC 827
Db 689 TCTGACACAATATATGAGATGACAGCTTCACTGATCTGTGAGAGAGAGATATGCTCG 748
QY 828 CCGCTTCAACATTTGCGCAAGAAAGCAATATGCTGATTTATGCGCGCAATGTTCC 885
Db 749 CCGGTTCTCAAACTGCGCAAGAGCTCAAACTATCTCTACTGCTCCCAACCTGAGC 806

RESULT 38
CNS0A44C 1401 bp mRNA linear HTC 06-FBB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSTPFB32FP01 of flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
ACCESSION BX826506.1 GI:42461918
VERSION 1
KEYWORDS HTC; GST cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1401)
Castelli V., Aury J.M., Jallion O., Wincker P., Clepet C.,
Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,
Temple G., Caboche M., Weissenbach J. and Salanoubat M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 1401)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Séquençage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
Genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
Length
http://www.genoscope.cns.fr/cgi-bin/gsb/gsb?source=Arabidopsis.
FEATURES
source
1..1401
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSTPFB32FP01"
/tissue_type="flowers and buds"
/plasmid="pCMVSPORT 6"
complement(1..1401)
/gene="At4g27585"

ORIGIN
Query Match 14.8%; Score 140.4; DB 3; Length 1401;
Best Local Similarity 49.3%; Pred. No. 2,1e-30;
Matches 427; Conservative 0; Mismatches 406; Indels 33; Gaps 1;

QY 65 TCCCCAGAGAGATCAAGTGTGAAAGGCTCGGCGTTCCATCGCGCTGACGG 124
Db 212 TTCGGAGAGAGAGGCGTTGTATTACGCAATTCGTAATACCTACGAGTGGCGT 271
QY 125 CCGGTTGAATTTTGAATTCCTTTATGACCGCGCTGACCGCATTCGCTGAAG 184
Db 272 CCGGATTCATTTCTCATTTCCGTTTCGTGAGATGATGCTTAATGCAATCTCTCAAG 331
QY 185 AATATCCTTTAAGCAATCCAGCAGCTGTCATCAACGCGCATTAATGCAATGACTG 244
Db 332 AAGAGCAATCCGATTCGAAATCAGACTGCGATTCTAAGCAACGTTAGATTCACA 391
QY 245 TTGACCGCATCTATTATTTCAAGTAACGATCCCAACTGCGCTCATACGTTGAGCA 304
Db 392 TCGATGTGTCTCTACGTAAGAGATGATGATCTTAAGTCAAGTCTTATGCGGTGAGA 451
QY 305 ACTACATTATGCAATTTACCGCTTCCCAACGAGCGTGGCTTCCTTATCGGCGCA 364
Db 452 GTCTATCTATCTGTGTGACGTGCTCAACCAACATGAGTGTGAGTGTGAGAG 511
QY 365 TGGAGTTGACAAAGCTTGAAGAACGCAAGAAATCAACAGTACCGTCTCTCGCC 424
Db 512 TCATCTTTATTAAGACTTTGAGAACGAAACTCTCAACGAAAGATGAGGAAGCA 571
QY 425 TCGATGACCGCGCGGCTGAGTGAAGTCTCTGTTACGAATCAAGATTTGG 484
Db 572 TCAATGTTCTGCAAAACACTGGGGGCTTCAGTGCCTGTTATGATGAGATGAGATATTA 631

Qy 485 TTCCCGCCGAAAGAAATCCTTGCAGCAATGCAAGCAAAATTAACGCCGCAACCGGAAAAAC 544
Db 632 TGCCCCCTCATGAGATGCGTGTCTATGAAATCAAGTGAAGCTGAGCGTAAAGAGT 691
Qy 545 GCGCCCGATTTGCGCAATCCGAAAGCCGTAATAATCGAAATCAATCACTTTCAGTGTTC 604
Db 692 GAGCCCAATCTTGAAGTCTGAAGGAAAGAAATCCCATATCAATCTGATGAGTA 751
Qy 605 AGCGTGAAGCCGAAATCCAAACATCCGAAGCGAGGCTCAGGCTCGGCTCAATGCGTCA 664
Db 752 AGAAAAAGTCTGTATCTTGGCATCTGAA----- 780
Qy 665 ATGCGGAGAAAAATGCGCCGATCAACCGCGCCAAAGCGAAAGCGAATCCCTGCGCCTTG 724
Db 781 --GCAGCAAGATGAGACGAGTGAATCGAGCAAGAGGAGGAGAAACAAATACACTA 838
Qy 725 TTGCGGAGCCAAATGCCAAGCAATCCGATCAATTTGCCCGCGCCCTTCAAAACCAAGCG 784
Db 839 GAGTACAAAGCTACTGCGAAAGGCTGATCTTGTCTTAACTCTCTCAAGAAACTGAGG 898
Qy 785 GGGCGGATGCGGTCATCTGAAGATTTGGGAAACAATACGTAGCCGCTTCAACAATCTTG 844
Db 899 GAGTGAAGGCGCGGCGGATTTGAGATTTGCAAGCAATACATACAGCTTTCGTAACATTG 958
Qy 845 CCAAGAAAGCAATACGCTGATTAATGCGCCCAATGTTGCGCAATCGGCAAGCCTGATT 904
Db 959 CCAAGAGGATACGATATTTGCTTCAAGTGTGCTTCAAAATCTCTAGCATGATTT 1018
Qy 905 CTGCGCGATGAAATTTATCGACAGC 930
Db 1019 CTCAAGCTTTAACAATGTAACAAAGC 1044

RESULT 39
CNS09PCR
LOCUS
DEFINITION
Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae local adult females. 5-PRIME end of clone
FROAC53BE07 of strain 6-9 of Anopheles gambiae (African malaria mosquito).
BX068923
VERSION
BK068923.1 GI:27642204
KEYWORDS
SOURCE
ORGANISM
Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
1 (bases 1 to 924)
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - web : www.genoscope.cns.fr)
Location/Qualifiers
1..924
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FROAC53BE07"
/plasmid="PME18S-FL"
/note="end : 5-PRIME"

ORIGIN
Query Match 14.7%; Score 139.6; DB 3; Length 924;
Best Local Similarity 53.9%; Pred. No. 3.3e-30;
Matches 329; Conservative 0; Mismatches 279; Indels 2; Gaps 2;

Qy 125 CCGGTTGAATATTTGATCCCTTATCGACCGCGTGCCTACCGCATTCGCTGAAG 184
Db 2 CCGGCTGAAGCTCTGCTGCGCGTGTGACCGGGTGAAGTGAAGTGAAGG 61

Qy 185 AAATCCCTTTAGACGTACCAACCCAGGCTGTGATCAGCCGCGATTAATCCGATTTGACTG 244
Db 62 AAATCGCAATPAGAGTGCAGCAAGTCCGCAATCAGTCCGCAACAGTAACTGACGA 121
Qy 245 TTGAGCGCATCATCTATTTCCAAATACCAATCCCAATCCGCTCATACGCTTCGAGCA 304
Db 122 TCGAGGCTGTCTTACCTGCGATTTCTGACCCGTAACCTGCGTGTGAGTGAAG 181
Qy 305 ACTACATTAATGCAATTAACCAAGCTTGCAGCAAGCAAGCAAGCTGCTTCCGTTATCCGAGTGA 364
Db 182 ACCCGAGTTTGCATCACCAGCTGCGCCAAAGAGATGCGCTCCGAGCTGGGCAAGA 241
Qy 365 TGAAGTTGACAAAACGTTTGAGAACGCGCAAGATTAACAGTACCTGTCTCCGCC 424
Db 242 TGTCACTGACAAAGGTCTCGAGAGCGCGATGCTCAACATCAGCATCGTGAAGTGA 301
Qy 425 TTGATGAAGCGCGCGGCTTGGGCTGTGAAGTCTCCGTTAGAAATCAAGATTTGG 484
Db 302 TC-AAAGAGGAGAGCAAGGCGGCAATCTCTGCTGCGGTACGAAATCCGCAATCA 360
Qy 485 TTCCGCGCAAGAAATCTCTTCGCAATGCAAGCAAAATTAACCGCGCAACGCGAAAAAC 544
Db 361 AGCTGCGAGCGCGGCTGCAAGAGCATGCAATGCAAGTGAAGCGGCG-CAAGC 419
Qy 545 GCGCCGATTTGCGGAATCCGAAGCGCGTAATAATGAACAATCACTTCCAGTGTG 604
Db 420 GGGCGGATCTCTGATCGAGGAGTGTCCGCGCGCGCATTAACGTGCGCAAGGTA 479
Qy 605 AGCGTGAAGCGGAATCCCAATCCGAAGCGGAGGCTCAGGCTGCGTCAATGCGTCA 664
Db 480 AGCAGAGTGCAGATCTTCTCGAGGCGGAGGAGAGAGAGATCAATGCGGCGA 539
Qy 665 ATGCGGAAATATCGCCGATCAACCGCGCAAGCGCAAGCGGAATCCCTGCGCCTTG 724
Db 540 ATGCTGAAGCGCGCGCATCATATGCGCGCATGCGCGTGCAGAAAGTGAATAATCG 599
Qy 725 TTGCGGAGC 734
Db 600 TGCGCGAATC 609

RESULT 40
AV434570
LOCUS
DEFINITION
AV434570 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone
PM045a11 x 5', mRNA sequence.
AV434570
ACCESSION
AV434570.1 GI:8589795
KEYWORDS
SOURCE
ORGANISM
Porphyra yezoensis
Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
1 (bases 1 to 528)
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
DNA Res. 7, 223-227 (2000)
20363100
10907854
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..528
/organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
/db_xref="taxon:2788"
/clone="PM045a11_x"

FEATURES
source

/clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

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Query Match      14.7%; Score 139.4; DB 1; Length 528;  
Best Local Similarity 55.2%; Pred. No. 3.2e-30;  
Matches 272; Conservative 0; Mismatches 221; Indels 0; Gaps 0;  
  
OY 62 TCATCCCCCAGAGAGAAATGCAAGTGTGCAAAAGGCTCGGCGTTTCATCGGCCCTGA 121  
   |||||  
Db 36 TCGTCCCCCAGAGAGAGGCGGATGTGAGCGCTTGTGCTTCCACCGCAAGCTGG 95  
   |||||  
OY 122 CGGCGCGTTGAATTTTGATTCCCTTATGACCGCGTCCCTACCGCATTGCTGA 181  
   |||||  
Db 96 AGCCCGGCTGAACTGGAATTATCCCTGTGTGACCAAGSTCAAGTACATCCACTCGTA 155  
   |||||  
OY 182 AAGAAATCCCTTAAGACGTACCCAGCGAGTCTGCATCAAGGCGGCGATATAGCAATTGA 241  
   |||||  
Db 156 AGGAGAGGCGCATTTGATTCTTAATCAAGTGGCCATCACCGGAGCAAGTGTCAATCA 215  
   |||||  
OY 242 CTGTGAGCGGCATCTATTTTCAAGTAACGATCCCAACTCGCTCATACGGTTTCA 301  
   |||||  
Db 216 ACCTGACGCAATTTCTGTTGCTCGGTGGAAGACCGGCTCAAGGCTGTGTAAGGAGTGG 275  
   |||||  
OY 302 GCAACTACATTATGCAATTACCCAGCTTGCCCAAGACGCTGCGTTCCGTTATCGGCG 361  
   |||||  
Db 276 AAAACCCGCGCAGGCGCATCACCTCTCGTCAAGACGATGCGCTCCGAGCTAGGAA 335  
   |||||  
OY 362 GTATGAGTGTGACAAAAGCTTTGAAGAACGCAAGAAATCAACGATACCGTCTCTCCG 421  
   |||||  
Db 336 AGCTCACTTGGACAAGACCTTCGAGAGCGGAGAGCCTCAACGCGGTATTGTCTCGT 395  
   |||||  
OY 422 CCCTGATGAGCGCGCGGCGCTTGGGAGTGTGAAAAGTCTCTCGTTACGAATCAAGGATT 481  
   |||||  
Db 396 CCATTAAAGCGCGCTGCGGAGGTTTGGGAGCATCACTGCGCTATGAAATCCGCGACA 455  
   |||||  
OY 482 TGGTTCCGCGCGCAAGAAATCTTCCGCAATGCAAGGACAAATTACCGCGCAACGCGAAA 541  
   |||||  
Db 456 TCTCCCGCGCGCCCAAGCGTGGCAAGGCGATGGAAGTCAAGCCGAAGCCGAACGCGCA 515  
   |||||  
OY 542 AACGGCGCCGCTAT 554  
   |||||  
Db 516 AGCGGCGCTCAGAT 528  
   |||||
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Search completed: August 14, 2005, 01:44:51
Job time : 3/51 secs

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PT vaccines and diagnostics.
XX Example 1; Page 76-77; 1453bp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to *Neisseria*
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 948 BP; 245 A; 278 C; 226 G; 199 T; 0 U; 0 Other;
Query Match 100.0%; Score 948; DB 3; Length 948;
Best Local Similarity 100.0%; Pred. No. 5e-276;
Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAATTTTTCATATCTTGTGGCAGCCGCGCTTTGCGCTTCAAAATCCTTTGTC 60
DB 1 ATGGAATTTTTCATATCTTGTGGCAGCCGCGCTTTGCGCTTCAAAATCCTTTGTC 60
QY 61 GTATCCCCCAGAGAAAGTCCAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCCTG 120
DB 61 GTATCCCCCAGAGAAAGTCCAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCCTG 120
QY 121 ACGGCGGTTTGAATTTTGAATTCCTTATCGACGCGTCCCTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATTTTGAATTCCTTATCGACGCGTCCCTACCGCATTCGCTG 180
QY 181 AAAGAAATCCCTTGAAGTGAAGTCCAGAGCTCTGCATACGCGCATATACGAATG 240
DB 181 AAAGAAATCCCTTGAAGTGAAGTCCAGAGCTCTGCATACGCGCATATACGAATG 240
QY 241 ACTGTTAGCGGATCATCTATTTCCAGTAACCGATCCCAAACTGCGCTCATACGCTTG 300
DB 241 ACTGTTAGCGGATCATCTATTTCCAGTAACCGATCCCAAACTGCGCTCATACGCTTG 300
QY 301 AGCAACTACATTAATGGAATTAACCAAGTTCGCGCAAGAGCGCTTCCGTTATCGGG 360
DB 301 AGCAACTACATTAATGGAATTAACCAAGTTCGCGCAAGAGCGCTTCCGTTATCGGG 360
QY 361 CGTATGAGTGAAGCAAAAGCTTTGAAGACGCGAAGATCAACAGTACCGTCTCC 420
DB 361 CGTATGAGTGAAGCAAAAGCTTTGAAGACGCGAAGATCAACAGTACCGTCTCTCC 420
QY 421 GCCCTCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTCTCCGTTACGAATCAAGAT 480
DB 421 GCCCTCGATGAAGCGCGCGGCTTGGGGTGTGAAGTCTCTCCGTTACGAATCAAGAT 480
QY 481 TTGTTTCCGCGCAAAATCTTTGCGCATGCGGCAAAATTAACCGCAAGCGCA 540
DB 481 TTGTTTCCGCGCAAAATCTTTGCGCATGCGGCAAAATTAACCGCAAGCGCA 540
QY 541 AAACGCGCCGATTTGCGCAATCCGAAGCGCTTAATTCGAACAATCAACCTTGCCAGT 600
DB 541 AAACGCGCCGATTTGCGCAATCCGAAGCGCTTAATTCGAACAATCAACCTTGCCAGT 600
QY 601 GGTGAGCTGAAGCGCAAAATCCGAAGCTCGAGGCTCAGGCTCGGTCATGCG 660
DB 601 GGTGAGCTGAAGCGCAAAATCCGAAGCTCGAGGCTCAGGCTCGGTCATGCG 660
QY 661 TTCATGCGGGAATGCGCGCATCAACGCGCGCAAGCGGAAGCGGAATCCTTGCGC 720
DB 661 TTCATGCGGGAATGCGCGCATCAACGCGCGCAAGCGGAAGCGGAATCCTTGCGC 720

QY 721 CTGTGTCGAAGCAATGCCGAAGCATCCGTCAAATTCGCGCGCCCTTCAAAACCAA 780
DB 721 CTGTGTCGAAGCAATGCCGAAGCATCCGTCAAATTCGCGCGCCCTTCAAAACCAA 780
QY 781 GCGCGGCGGATGCGGTCAATCTGAACATTTGCGGAACAAATCGTACCGCTTCAACAT 840
DB 781 GCGCGGCGGATGCGGTCAATCTGAACATTTGCGGAACAAATCGTACCGCTTCAACAT 840
QY 841 CTGCGCAAAAGCAATACGCTGATTATGCGCCGCAATGTTGCGCAATCGCAGCCTG 900
DB 841 CTGCGCAAAAGCAATACGCTGATTATGCGCCGCAATGTTGCGCAATCGCAGCCTG 900
QY 901 ATTCTGCGCGCATGAATTTATGACAGCAGCAAAACCGCAATTA 948
DB 901 ATTCTGCGCGCATGAATTTATGACAGCAGCAAAACCGCAATTA 948
RESULT 2
AA253752
ID AA253752 standard; DNA; 948 BP.
XX
AC AA253752;
XX
DT 15-SEP-2003 (revised)
DT 21-MAR-2000 (first entry)
DE *Neisseria gonorrhoeae* ORF 519 partial DNA sequence SEQ ID NO:1453.
XX
KM *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy; ds.
XX
OS *Neisseria gonorrhoeae*.
XX
EN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M,
PI Petersen J, Pizza M, Rappuoli R, Ratzi G, Scalato E, Scarselli M,
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR P-PSDB: AAY74990.
XX
PT Novel *Neisseria* polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 7; Page 778-779; 1453bp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to *Neisseria*
CC bacteria (e.g. meningitis and septicemia), to detect the presence of

CC Neisseria bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
 CC field)

XX Sequence 948 BP, 245 A, 278 C, 226 G, 199 T, 0 U, 0 Other;

Query Match 100.0%; Score 948; DB 3; Length 948;
 Best Local Similarity 100.0%; Pred. No. 5e-276;
 Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGGAATTTTTCATTATCTTGTGGCAGCCGCTTTCGGCTTCAATCCTTTGTC 60
DB 1 ATGGAATTTTTCATTATCTTGTGGCAGCCGCTTTCGGCTTCAATCCTTTGTC 60
QY 61 GTTCATCCCCCAGAGAGATCCACGCTGTCGAAAGGCTGGGCGTTTCATGCGCCCTG 120
DB 61 GTTCATCCCCCAGAGAGATCCACGCTGTCGAAAGGCTGGGCGTTTCATGCGCCCTG 120
QY 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGCGCTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGCGCTACCGCATTCGCTG 180
QY 181 AAAAAGATCCCTTTAGACGTACCCAGCCAGCTGTGATCAACGGCGATTAATACGCAATTG 240
DB 181 AAAAAGATCCCTTTAGACGTACCCAGCCAGCTGTGATCAACGGCGATTAATACGCAATTG 240
QY 241 ACTGTTGAAGGAGATCATCTATTTCAGAGTACCGATCCCAACTGCTCATACGAGTTG 300
DB 241 ACTGTTGAAGGAGATCATCTATTTCAGAGTACCGATCCCAACTGCTCATACGAGTTG 300
QY 301 AGCAATCACTATATGCAATTAACCCAGCTTGCACCAACGACGCTGCTTATCGAG 360
DB 301 AGCAATCACTATATGCAATTAACCCAGCTTGCACCAACGACGCTGCTTATCGAG 360
QY 361 CGTATGAGTTTGAACAAACGTTTGAAGAACGACGAATCAACGTAACCGTCTC 420
DB 361 CGTATGAGTTTGAACAAACGTTTGAAGAACGACGAATCAACGTAACCGTCTC 420
QY 421 GCCCTCGATGAAGACCGCGCGCTTGGGGGTGAAGTCTCCGTTACGAATCAAGAT 480
DB 421 GCCCTCGATGAAGACCGCGCGCTTGGGGGTGAAGTCTCCGTTACGAATCAAGAT 480
QY 481 TTGGTTCCGCGCGCAAGAAATCCTTCGCGCAATGACAGCAAAATTAACCGCGCA 540
DB 481 TTGGTTCCGCGCGCAAGAAATCCTTCGCGCAATGACAGCAAAATTAACCGCGCA 540
QY 541 AAAACGCGCCGTAATTCGCGCAATCGAAGCGCGTAAATGCAACAAATCAACCTTGCAGT 600
DB 541 AAAACGCGCCGTAATTCGCGCAATCGAAGCGCGTAAATGCAACAAATCAACCTTGCAGT 600
QY 601 GGTGACGCTGGAAGCCGAATTCGAACATCGAAGGGGAGGCTGAGCTGGCGTATGGG 660
DB 601 GGTGACGCTGGAAGCCGAATTCGAACATCGAAGGGGAGGCTGAGCTGGCGTATGGG 660
QY 661 TCCATGCGGAGAAATTCGCGCGCATCAACCGCGCAAAAGGCGAAGCGAATCCTGCGC 720
DB 661 TCCATGCGGAGAAATTCGCGCGCATCAACCGCGCAAAAGGCGAAGCGAATCCTGCGC 720
QY 721 CTTGTTGCGGAGCCCAATGCGGAGCGATCGTCAAAATTCGCGCGCTTCAAAACCA 780
DB 721 CTTGTTGCGGAGCCCAATGCGGAGCGATCGTCAAAATTCGCGCGCTTCAAAACCA 780
QY 781 GGGGGGGCGGATCGGTCATCTGAAGATTGGCGAAACAAATACGAGCGGTTCAACAT 840
DB 781 GGGGGGGCGGATCGGTCATCTGAAGATTGGCGAAACAAATACGAGCGGTTCAACAT 840
QY 841 CTGCGCAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGACATCGGAGCGCTG 900
DB 841 CTGCGCAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGACATCGGAGCGCTG 900
QY 901 ATTTGCGCGCATGAAATTAATGACAGCAAGCAAAACCGCCCAATTA 948
  
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DB 901 ATTTGCGCGCATGAAATTAATGACAGCAAGCAAAACCGCCCAATTA 948

RESULT 3
 AAA81267

ID AAA81267 standard; DNA; 948 BP.

XX AAA81267;

XX 15-SEP-2003 (revised)
 DT 04-DEC-2000 (first entry)

XX N. gonorrhoeae partial DNA sequence g519-1.seq SEQ ID NO:976.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; Memb; ds.

XX Neisseria gonorrhoeae.

XX WO200022430-A2.

XX 20-APR-2000.

XX 08-OCT-1999; 99WO-US023573.

XX 09-OCT-1998; 98US-0103794P.

XX 30-APR-1999; 99US-0132068P.

XX (CHIR) CHIRON CORP.

XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC,
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
 PI Rappelli R, Pizzo M;

XX WPI: 2000-318079/27.
 DR P-PSDB; AAB25627.

PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.

XX Claim 9; Page 73-74; 1760bp; English.

XX The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions. (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 948 BP, 245 A, 278 C, 226 G, 199 T, 0 U, 0 Other;

Query Match	100.0%;	Score 948;	DB 3;	Length 948;
Best Local Similarity	100.0%;	Pred. No. 5e-276;		
Matches 948;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAATTTTCATTAATCTTGTGGAGCCGTCGCGCTTTGGCTTCAATCCTTTGTC	60	
DB	1	ATGGAATTTTCATTAATCTTGTGGAGCCGTCGCGCTTTGGCTTCAATCCTTTGTC	60	
QY	61	GTCAATCCCGCAGAGAGTCCAGCTTGTGAAAAGCTCGGGCGTTTCATCGGCGCTG	120	
DB	61	GTCAATCCCGCAGAGAGTCCAGCTTGTGAAAAGCTCGGGCGTTTCATCGGCGCTG	120	
QY	121	ACGGCCGGTTTGAATATTTTGAATTCCTTTATCGACCGGTCGCTTACCGCATTCGCTG	180	
DB	121	ACGGCCGGTTTGAATATTTTGAATTCCTTTATCGACCGGTCGCTTACCGCATTCGCTG	180	
QY	181	AAAGAAATCCCTTTAGAGTACCCAGCCAGCTCTGCATACGCGGATATACGCAATTCG	240	
DB	181	AAAGAAATCCCTTTAGAGTACCCAGCCAGCTCTGCATACGCGGATATACGCAATTCG	240	
QY	241	ACTGTTGACGGCATCATTAATTTTCAAGTAAACGATCCCAAACTGCGCTCATACGGTTTCG	300	
DB	241	ACTGTTGACGGCATCATTAATTTTCAAGTAAACGATCCCAAACTGCGCTCATACGGTTTCG	300	
QY	301	AGCAACTACATTAATGCAATTAACCAAGCTTCCCAAGACGCTGCTTCCGTTATTCGGG	360	
DB	301	AGCAACTACATTAATGCAATTAACCAAGCTTCCCAAGACGCTGCTTCCGTTATTCGGG	360	
QY	361	CGTATGAGTTTGACAAACGTTTGAAGACGCGACGAATTAACAGTACCGTCTTC	420	
DB	361	CGTATGAGTTTGACAAACGTTTGAAGACGCGACGAATTAACAGTACCGTCTTC	420	
QY	421	GCCCTCGATGAAGCCGCGGGGCTTGGGGGTGAAAGTCCCTCGTTAAGAAATCAAGAT	480	
DB	421	GCCCTCGATGAAGCCGCGGGGCTTGGGGGTGAAAGTCCCTCGTTAAGAAATCAAGAT	480	
QY	481	TTGGTTCCGCGCAAGAAATCCTTCGCGCATGACGACCAAAATTAACGCGCAACGCGAA	540	
DB	481	TTGGTTCCGCGCAAGAAATCCTTCGCGCATGACGACCAAAATTAACGCGCAACGCGAA	540	
QY	541	AAAGCGCCGCTATTTGCGGAATCCGAAGCCGTAATAATGAACAAATCACTTCCAGT	600	
DB	541	AAAGCGCCGCTATTTGCGGAATCCGAAGCCGTAATAATGAACAAATCACTTCCAGT	600	
QY	601	GCTCAGCGTGAAGCCGAATCCCAATCCGAAGCGAGGCTCAGGCTCGGCTCAATGCG	660	
DB	601	GCTCAGCGTGAAGCCGAATCCCAATCCGAAGCGAGGCTCAGGCTCGGCTCAATGCG	660	
QY	661	TCCAAATGCGAGAAATCGCCGCAATCAACGCGCCAAAGGCGAAATCCCTGCGC	720	
DB	661	TCCAAATGCGAGAAATCGCCGCAATCAACGCGCCAAAGGCGAAATCCCTGCGC	720	
QY	721	CTTGTTCGCGAAGCCCAATCCGATCCGTAATTCGCGCGCTTCAAAACCA	780	
DB	721	CTTGTTCGCGAAGCCCAATCCGATCCGTAATTCGCGCGCTTCAAAACCA	780	
QY	781	GCGCGGGCGAGTCCGCTCAATCGAAGATGCGGAACATATGTAAGCGCGTTCAACAT	840	
DB	781	GCGCGGGCGAGTCCGCTCAATCGAAGATGCGGAACATATGTAAGCGCGTTCAACAT	840	
QY	841	CTTGCCTAAGAAAGATACGCTGATTAATGCGCGCAATGTTCCGACATCGGACGCTG	900	
DB	841	CTTGCCTAAGAAAGATACGCTGATTAATGCGCGCAATGTTCCGACATCGGACGCTG	900	
QY	901	ATTTCTGCGCGATGAATAATTAATGACAGCAGCAAAACCGCCAAATTA	948	
DB	901	ATTTCTGCGCGATGAATAATTAATGACAGCAGCAAAACCGCCAAATTA	948	

RESULT 4
AAF21552
ID AAF21552 standard; DNA; 948 BP.
XX

AC	AAF21552;
XX	
DT	15-SEP-2003 (revised)
DT	13-MAR-2001 (first entry)
XX	
DE	N. gonorrhoeae partial DNA sequence g519-1.seq SEQ ID NO:16.
XX	
KW	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW	diagnosis; antigen; detection; infection; gene therapy; antibacterial;
KW	ds.
OS	Neisseria gonorrhoeae.
XX	
PN	MO20006791-A1.
PD	09-NOV-2000.
XX	
PF	08-MAR-2000; 2000MO-US005928.
XX	
PR	30-APR-1999; 99US-0132068P.
PR	08-OCT-1999; 99MO-US023573.
PR	28-FEB-2000; 2000GB-00004695.
XX	
PA	(CHIR) CHIRON CORP.
XX	(GENO-) INST GENOMIC RES.
PI	Pizza M, Hickey E, Peterson J, Tettein H, Venter JC;
PI	Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI	Rappuoli R, Frazer CM, Grandi G;
DR	WPI; 2000-647603/62.
XX	P-PSDB; AAB58557.
PT	Neisseria meningitidis B full length genome sequence and open reading
PT	frames are used to detect, treat and prevent Neisserial infections.
XX	
PS	Example 1; Page 74; 692pp; English.
XX	
CC	The present invention describes the full length genome of Neisseria
CC	meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC	represent fragments of the NMB genomic sequence, as the sequence was too
CC	long to go in a record on its own it was split into 8 sequences which
CC	overlap each other at the beginning and end of each sequence by 4980 bp
CC	(i.e. the last 4980 bp of AAF21544 is repeated at the beginning of
CC	AAF21607, the last 4980 bp of AAF21607 are repeated at the beginning of
CC	AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC	given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC	primers which are used in the exemplification of the present invention.
CC	The NMB genome and fragments from it have antibacterial activity, and can
CC	be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC	and/or antibodies which binds to the proteins can be used in compositions
CC	for treating or preventing infection due to Neisserial bacteria or as a
CC	diagnostic reagent for detecting the presence of Neisserial bacteria or
CC	of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC	computer storage medium or computer databases can be used in a search to
CC	identify open reading frames (ORFs) or coding sequences within the NMB
CC	genome. The DNA sequences provide further opportunities to find antigenic
CC	or immunogenic proteins which are more effective in vaccines than the
CC	outer membrane proteins currently used. (Updated on 15-SEP-2003 to
XX	standardise OS field)
XX	
SQ	Sequence 948 BP; 245 A; 278 C; 226 G; 199 T; 0 U; 0 Other;
Query Match	100.0%; Score 948; DB 3; Length 948;
Best Local Similarity	100.0%; Pred. NO. 5e-276;
Matches 948; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGAATTTTCATTAATCTTGTGGAGCCGTCGCGCTTTGGCTTCAATCCTTTGTC 60
DB	1 ATGGAATTTTCATTAATCTTGTGGAGCCGTCGCGCTTTGGCTTCAATCCTTTGTC 60
QY	61 GTCAATCCCGCAGAGAGTCCAGCTTGTGAAAAGCTCGGGCGTTTCATCGGCGCCTG 120


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Db      61  GTGATCCCCGACGAAAGTCCAGTGTGCGAAAGGCTCGGGCGTTTCATCGGCCCTG 120
Oy      121  ACGGCGGTTTGAATATTTTGAATTCCTTTATGACCGCGGTGCGCTACCGCATTCGCTG 180
Db      121  ACGGCGGTTTGAATATTTTGAATTCCTTTATGACCGCGGTGCGCTACCGCATTCGCTG 180
Oy      181  AAGAAATTCCTTTAGAGTACCGACCGCGGTGCTGATCAGACCGGATTAATGCAATTG 240
Db      181  AAGAAATTCCTTTAGAGTACCGACCGGTGCTGATCAGACCGGATTAATGCAATTG 240
Oy      241  ACTGTGACGCGCATCTATTTCGAAGTAACGATCCCAATCTGCGCTCATACGATTG 300
Db      241  ACTGTGACGCGCATCTATTTCGAAGTAACGATCCCAATCTGCGCTCATACGATTG 300
Oy      301  AGCAACTATATGCAATTAACCAAGCTTGGCCCAACGACGCTGCTTCCGTTATCGGG 360
Db      301  AGCAACTATATGCAATTAACCAAGCTTGGCCCAACGACGCTGCTTCCGTTATCGGG 360
Oy      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGACGAAATCAACAGTACCGTCTGCTC 420
Db      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGACGAAATCAACAGTACCGTCTGCTC 420
Oy      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCTGTTACGAAATCAAGAT 480
Db      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCTGTTACGAAATCAAGAT 480
Oy      481  TTGGTTCCGCGCGCAAGAAATCCTTCGCGCAATGCAAGCAAAATTAACGCGCAACGCG 540
Db      481  TTGGTTCCGCGCGCAAGAAATCCTTCGCGCAATGCAAGCAAAATTAACGCGCAACGCG 540
Oy      541  AAACGCGCGGTTATTCGCAATCCGAAGCCGTTAAATGGAACAAATCAACCTTGGCAAT 600
Db      541  AAACGCGCGGTTATTCGCAATCCGAAGCCGTTAAATGGAACAAATCAACCTTGGCAAT 600
Oy      601  GGTGACGCGGAAAGCGGAAATCCAAATCCGAAGGCGGAGGCTCAGGCTGCGTCAATGCG 660
Db      601  GGTGACGCGGAAAGCGGAAATCCAAATCCGAAGGCGGAGGCTCAGGCTGCGTCAATGCG 660
Oy      661  TCCAAATGCGGAAATTCGCGCGCATCAACCGCGCCAAAGCGGAGCGGAAATCCCTGCGC 720
Db      661  TCCAAATGCGGAAATTCGCGCGCATCAACCGCGCCAAAGCGGAGCGGAAATCCCTGCGC 720
Oy      721  CTTGTTGCGGAAGCCATGCGCGCATTCGCAATTCGCGCGCTTCAAAACCA 780
Db      721  CTTGTTGCGGAAGCCATGCGCGCATTCGCAATTCGCGCGCTTCAAAACCA 780
Oy      781  GCGCGGGCGGATCGGTCATCTGAAGTTGCGGAAATCAATGCTAGCGGCTTCAACAT 840
Db      781  GCGCGGGCGGATCGGTCATCTGAAGTTGCGGAAATCAATGCTAGCGGCTTCAACAT 840
Oy      841  CTTGCGAAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCCGACATCGGCAAGCTG 900
Db      841  CTTGCGAAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCCGACATCGGCAAGCTG 900
Oy      901  ATTTCGCGCGCATGAAATTTATGACAGACGCAAAAACCGCCAAATTA 948
Db      901  ATTTCGCGCGCATGAAATTTATGACAGACGCAAAAACCGCCAAATTA 948

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RESULT 5
ABZ40185
ID ABZ40185 standard; DNA; 945 BP.

XX ABZ40185;

XX 07-MAR-2003 (first entry)

XX N. gonorrhoeae nucleotide sequence SEQ ID 4959.

XX Antibacterial; infection; vaccine; gene therapy; gene; ds.

XX OS Neisseria gonorrhoeae.

XX

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PN      W0200279243-A2.
PD      10-OCT-2002.
XX      PF 12-FEB-2002; 2002WO-IB002069.
XX      PR 12-FEB-2001; 2001GB-00003424.
XX      PA (CHIR-) CHIRON SPA.
XX      PI Fontana MR, Pizza M, Masignani V, Monaci E;
XX      DR WPI: 2003-058415/05.
XX      DR P-PSDB; ABP79215.
PT      New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PS      medicament for treating or preventing N. gonorrhoeae infection.
        Disclosure; Page 551; 815pp; English.
CC      The present invention relates to proteins from Neisseria gonorrhoeae.
CC      Also disclosed are the nucleic acid molecules encoding the proteins and
CC      antibodies that specifically bind to the proteins. The composition
CC      comprising the protein, nucleic acid or antibody is useful for the
CC      manufacture of a medicament for treating or preventing N. gonorrhoeae
CC      infection, this may be in the form of a vaccine or gene therapy.
CC      Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
CC      molecules of the invention
SQ      Sequence 945 BP; 243 A; 278 C; 226 G; 198 T; 0 U; 0 Other;

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Query Match 99.7%; Score 945; DB 10; Length 945;
Best Local Similarity 100.0%; Pred. No. 4e-275;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      1  ATGGAATTTTTCATTATCTTGTGGCAGCGCGCTTGGCTTCAATCCTTTGTC 60
Db      1  ATGGAATTTTTCATTATCTTGTGGCAGCGCGCTTGGCTTCAATCCTTTGTC 60
Oy      61  GTGATCCCCGACGAAAGTCCAGTGTGCGAAAGGCTCGGGCGTTTCCATGCGGCCCTG 120
Db      61  GTGATCCCCGACGAAAGTCCAGTGTGCGAAAGGCTCGGGCGTTTCCATGCGGCCCTG 120
Oy      121  ACGGCGGTTTGAATATTTTGAATTCCTTTATGACCGCGGTGCGCTACCGCATTCGCTG 180
Db      121  ACGGCGGTTTGAATATTTTGAATTCCTTTATGACCGCGGTGCGCTACCGCATTCGCTG 180
Oy      181  AAGAAATTCCTTTAGAGTACCGACCGGTGCTGATCAGACCGGATTAATGCAATTG 240
Db      181  AAGAAATTCCTTTAGAGTACCGACCGGTGCTGATCAGACCGGATTAATGCAATTG 240
Oy      241  ACTGTGACGCGCATCTATTTCGAAGTAACGATCCCAATCTGCGCTCATACGATTG 300
Db      241  ACTGTGACGCGCATCTATTTCGAAGTAACGATCCCAATCTGCGCTCATACGATTG 300
Oy      301  AGCAACTATATGCAATTAACCAAGCTTGGCCCAACGACGCTGCTTCCGTTATCGGG 360
Db      301  AGCAACTATATGCAATTAACCAAGCTTGGCCCAACGACGCTGCTTCCGTTATCGGG 360
Oy      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGACGAAATCAACAGTACCGTCTGCTC 420
Db      361  CGTATGAGTGTGACAAACGTTTGAAGAACCGACGAAATCAACAGTACCGTCTGCTC 420
Oy      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCTGTTACGAAATCAAGAT 480
Db      421  GGCCTGATGAAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCTGTTACGAAATCAAGAT 480
Oy      481  TTGGTTCCGCGCGCAAGAAATCCTTCGCGCAATGCAAGCAAAATTAACGCGCAACGCG 540
Db      481  TTGGTTCCGCGCGCAAGAAATCCTTCGCGCAATGCAAGCAAAATTAACGCGCAACGCG 540
Oy      541  AAACGCGCGGTTATTCGCAATCCGAAGCCGTTAAATGGAACAAATCAACCTTGGCAAT 600

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Db 541 AAACGCCCGCTATTGCGCATTCGAAAGCCGCTAAATCGAACCAATCACTTCGCACT 600
QY 601 GGTGACGCGTGAAGCCGAAATTCGAACATTCGAAAGGCGAGCTCAGGCTGCGGTCAATGCG 660
Db 601 GGTGACGCGTGAAGCCGAAATTCGAACATTCGAAAGGCGAGCTCAGGCTGCGGTCAATGCG 660
QY 661 TCCAAATGCGGAAATTCGCGCATCAACGCGCCAAAGGCGAAAGCGGAATCCCTGCGC 720
Db 661 TCCAAATGCGGAAATTCGCGCATCAACGCGCCAAAGGCGAAAGCGGAATCCCTGCGC 720
QY 721 CTGTTGCGGAAAGCCGCAATTCGCAATTCGCGCGCCCTTTAAACCCAA 780
Db 721 CTGTTGCGGAAAGCCGCAATTCGCAATTCGCGCGCCCTTTAAACCCAA 780
QY 781 GCGCGGCGGATGCGGTCAATTCGAAAGATTGCGGAAACATATGACCGCGTTCAACAT 840
Db 781 GCGCGGCGGATGCGGTCAATTCGAAAGATTGCGGAAACATATGACCGCGTTCAACAT 840
QY 841 CTGCGCAAGAAAGCAATACGCTGATTTATGCGCGCAATGTCGCAATCGGCAAGCTG 900
Db 841 CTGCGCAAGAAAGCAATACGCTGATTTATGCGCGCAATGTCGCAATCGGCAAGCTG 900
QY 901 ATTTCGCGGATGAAATTTATCGACAGCAGCAAAACCGCCAA 945
Db 901 ATTTCGCGGATGAAATTTATCGACAGCAGCAAAACCGCCAA 945

RESULT 6

AA253754
ID AA253754 standard; DNA; 948 BP.

AC AA253754;

DT 21-MAR-2000 (first entry)

DE Neisseria meningitidis ORF 519 partial DNA sequence SNU ID NO:1457.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KW antibacterial; gene therapy; ds.

OS Neisseria meningitidis.

XX WO957280-A2.

PN 11-NOV-1999.

XX 30-APR-1999; 99WO-US009346.

PF 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 09-OCT-1998; 98US-0103796P.

PR 25-FEB-1999; 99US-0121528P.

XX (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

XX Frazer C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

PI Petersen J, Pizzo M, Rappoli R, Ratti G, Scalato B, Scarselli M;

PI Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

DR P-PsDB; AAY74992.

XX Novel Neisserial polypeptides predicted to be useful antigens for

PT vaccines and diagnostics.

XX Claim 7, Page 780; 1453pp; English.

CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254617 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to *Neisseria*
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols

XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;

QY Query Match 93.9%; Score 890.4; DB 3; Length 948;

Db Best Local Similarity 96.2%; Pred. No. 1.3e-258;

QY Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 AAGGAATTTTCATTTATCTGTTGAGCGCGTCCGCTTTCGCTTCAATCTTGTG 60

Db 1 AAGGAATTTTCATTTATCTGTTGAGCGCGTCCGCTTTCGCTTCAATCTTGTG 60

QY 61 GTCAATCCCGCAGAGAAAGTCACGTTGTGAAAGGCTCGGCGTTTCATCGCGCCTG 120

Db 61 GTCAATCCCGCAGAGAAAGTCACGTTGTGAAAGGCTCGGCGTTTCATCGCGCCTG 120

QY 121 ACGCGCGTTTGAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 180

Db 121 ACGCGCGTTTGAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 180

QY 181 AAAGAAATCCCTTTAGAGATGATCCAGCGAGTCTGATCAAGCGATTAATACCAATTG 240

Db 181 AAAGAAATCCCTTTAGAGATGATCCAGCGAGTCTGATCAAGCGATTAATACCAATTG 240

QY 241 ACTGTTGACGCGATCATTTATTTTCAAGTAAACGATCCCAATCTGCTTATACGTTTG 300

Db 241 ACTGTTGACGCGATCATTTATTTTCAAGTAAACGATCCCAATCTGCTTATACGTTTG 300

QY 301 AGCAACTCATTTATTTGCAATTTACCAAGTTTCCCAACGAGCGTTCCTTATCGGG 360

Db 301 AGCAACTCATTTATTTGCAATTTACCAAGTTTCCCAACGAGCGTTCCTTATCGGG 360

QY 361 CGTATGAGTTGGAACAATTCCTTTCGCGCAATGCAAGGCAAAATTAACGCGGCA 420

Db 361 CGTATGAGTTGGAACAATTCCTTTCGCGCAATGCAAGGCAAAATTAACGCGGCA 420

QY 421 GCGCTCGATGAAAGCGCGCGGCTTGGGTTGAAAGTTTGGCTTATGAAATTAAGAC 480

Db 421 GCGCTCGATGAAAGCGCGCGGCTTGGGTTGAAAGTTTGGCTTATGAAATTAAGAC 480

QY 481 TTGTTTCCGCGGCAAGAAATTCCTTTCGCGCAATGCAAGGCAAAATTAACGCGGCA 540

Db 481 TTGTTTCCGCGGCAAGAAATTCCTTTCGCGCAATGCAAGGCAAAATTAACGCGGCA 540

QY 541 AAAGCGCGCGTATTTGCGGATTCGAAAGCGGTAATTCGAAACCAATCACTTGCACT 600

Db 541 AAAGCGCGCGTATTTGCGGATTCGAAAGCGGTAATTCGAAACCAATCACTTGCACT 600

QY 601 GGTGACGCGTGAAGCCGAAATTCGAACATTCGAAAGGCGAGCTCAGGCTGCGGTCAATGCG 660

Db 601 GGTGACGCGTGAAGCCGAAATTCGAACATTCGAAAGGCGAGCTCAGGCTGCGGTCAATGCG 660

QY 661 TCCAAATGCGGAAATTCGCGCATCAACGCGCCAAAGGCGAAAGCGGAATCCCTGCGC 720

Db 661 TCCAAATGCGGAAATTCGCGCATCAACGCGCCAAAGGCGAAAGCGGAATCCCTGCGC 720

QY 721 CTGTTGCGGAAAGCCGCAATTCGCAATTCGCGCGCCCTTTAAACCCAA 780

Db 721 CTGTTGCGGAAAGCCGCAATTCGCAATTCGCGCGCCCTTTAAACCCAA 780

QY 781 GCGCGGCGGATGCGGTCAATTCGAAAGATTGCGGAAACATATGACCGCGTTCAACAT 840

Db 781 GCGCGGCGGATGCGGTCAATTCGAAAGATTGCGGAAACATATGACCGCGTTCAACAT 840

XX AA254585;
AC 21-MAR-2000 (first entry)
XX DT
XX Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:3055.
DE
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
KM
XX Neisseria meningitidis.
OS
XX MO957280-A2.
PN
XX 11-NOV-1999.
PD
XX 30-APR-1999; 99WO-US009346.
PF
XX 01-MAY-1998; 98US-0083758P.
PR 31-JUN-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Peterson J, Pizzi M, Rapuoli R, Ratcl G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI; 2000-062150/05.
DR P-PSDB; AAY75783.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
XX Example 1; Page 77-78; 1453pp; English.
PS
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
XX represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
XX and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
XX PCR primers used in the exemplification of the present invention. The
XX polypeptides, the polynucleotides, antibodies and compositions of the
XX invention can be used as vaccines, as diagnostic reagents, and as
XX immunogenic compositions. The polypeptides can be used in the manufacture
XX of medicaments for treating or preventing infection due to Neisserial
XX bacteria (e.g. meningitis and septicemia), to detect the presence of
XX Neisseria bacteria, or to raise antibodies. They may also be used to
XX screen for agonists or antagonists, which may themselves have use as
XX antibacterial agents. The polynucleotides of the invention may also be
XX used in gene therapy protocols
XX
XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;
SQ
Query Match 93.9%; Score 890.4; DB 3; Length 948;
Best Local Similarity 96.2%; Pred. No. 1.3e-258;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

DB 121 ACGCCGGTTTGAATAATTTTGAATTCCTTTATCGACCGCGCTACCGCAATTCGCTG 180
QY 181 AAAGAAATCCCTTTAGACGTACCCAGCAGGCTGTCATACGCGCGATTAATACCAATTG 240
DB 181 AAAGAAATCCCTTTAGACGTACCCAGCAGGCTGTCATACGCGCGATTAATACCAAGT 240
QY 241 ACTGTTGACGGCATCATCTATTTTCCAGATACCGATCCAAATCGCCTCATACGTTTCG 300
DB 241 ACTGTTGACGGCATCATCTATTTTCCAGATACCGATCCAAATCGCCTCATACGTTTCG 300
QY 301 AGCAACTACATTAATGAGCAATTAACCCAGCTTCCCAACGACGCTGCTTATTCGGG 360
DB 301 AGCAACTACATTAATGAGCAATTAACCCAGCTTCCCAACGACGCTGCTTATTCGGG 360
QY 361 CGTATGAGTTGACAAACGTTTGAAGAACGCGACGCAATATCAACAGTACCGTCTCC 420
DB 361 CGTATGAGTTGACAAACGTTTGAAGAACGCGACGCAATATCAACAGTACCGTCTCC 420
QY 421 GCCCTGATGAAAGCCGCGCGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGAT 480
DB 421 GCCCTGATGAAAGCCGCGCGCTTGGGCTGTGAAGTCTCCGTTATGAGATTAAGAC 480
QY 481 TTGTTCCGCGCGCAAGAAATCTTTCGCGCAATGACGCACAATTAACCGCGCAAG 540
DB 481 TTGTTCCGCGCGCAAGAAATCTTTCGCGCAATGACGCGCAAAATTAAGTGAACGGGAA 540
QY 541 AAACGCGCGGATTTGGCGAATCCGAAGCGCGTAAATTCGAACAAATCAACTTCCAGT 600
DB 541 AAACGCGCGGATTTGGCGAATCCGAAGCGCGTAAATTCGAACAAATCAACTTCCAGT 600
QY 601 GGTGAGCGTGAAGCGCAATTCGAACAAATTCGAAGCGCGTCAAGCTGCGGTCAATGCG 660
DB 601 GGTGAGCGCGAAGCGCAATTCGAACAAATTCGAAGCGCGTCAAGCTGCGGTCAATGCG 660
QY 661 TCCAATGCCGCAAGAAATGCGCGCATCAACCGCGCAAGCGCAAGCGCAATTCCTGGC 720
DB 661 TCCAATGCCGCAAGAAATGCGCGCATCAACCGCGCAAGCGCAAGCGCAATTCCTGGC 720
QY 721 CTTGTTGCCGAAGCAATTCGCAAGCAATTCGCAATTCGCAATTCGCAATTCGCAATTC 780
DB 721 CTTGTTGCCGAAGCAATTCGCAAGCAATTCGCAATTCGCAATTCGCAATTCGCAATTC 780
QY 781 GCGCGGCGGATGCGGTCAATTCGAAGATTCGCAAGCAATTCGCAATTCGCAATTCG 840
DB 781 GCGCGGCGGATGCGGTCAATTCGAAGATTCGCAAGCAATTCGCAATTCGCAATTCG 840
QY 841 CTTGCGCAAGAAAGCAATTCGCTATTAATGCGCGCAATTCGCGCAATTCGCGCAATTC 900
DB 841 CTTGCGCAAGAAAGCAATTCGCTATTAATGCGCGCAATTCGCGCAATTCGCGCAATTC 900
QY 901 ATTCTGCGGATGAATAATTAATGACGACGCAAGAAACCGCAATTA 948
DB 901 ATTCTGCGGATGAATAATTAATGACGACGCAAGAAACCGCAATTA 948
RESULT 9
AA253751
ID AA253751 standard; DNA; 948 BP.
XX
XX AA253751;
AC 21-MAR-2000 (first entry)
XX DT
XX Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:1451.
DE
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
XX antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
KM
XX Neisseria meningitidis.
OS
XX MO957280-A2.
PN
XX

PD 11-NOV-1999.
 XX 30-APR-1999; 99WO-US009346.
 XX 01-MAY-1998; 98US-0083758P.
 PR 31-JUL-1998; 98US-0094869P.
 PR 02-SEP-1998; 98US-0098994P.
 PR 02-SEP-1998; 98US-0099062P.
 PR 09-OCT-1998; 98US-0103749P.
 PR 09-OCT-1998; 98US-0103794P.
 PR 09-OCT-1998; 98US-0103796P.
 PR 25-FEB-1999; 99US-0121528P.
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX Frazer C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tectelin H, Venter JC;
 DR WPI; 2000-062150/05.
 XX P-PSDB; AAY74989.
 PT Novel *Neisseria* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics.
 XX Claim 7; Page 777-778; 1453pp; English.
 PS AA254015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of the
 CC invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the manufacture
 CC of medicaments for treating or preventing infection due to *Neisseria*
 CC bacteria (e.g. meningitis and septicemia), to detect the presence of
 CC *Neisseria* bacteria, or to raise antibodies. They may also be used to
 CC screen for agonists or antagonists, which may themselves have use as
 CC antibacterial agents. The polynucleotides of the invention may also be
 CC used in gene therapy protocols
 XX
 XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;
 SQ
 Query Match 93.9%; Score 890.4; DB 3; Length 948;
 Best Local Similarity 96.2%; Pred. No. 1.3e-258;
 Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 1 ATGGAATTTTTCATTAATCTTGTGGCAGCCGCTGCGCTTTCGCTTCAAAATCCTTTGTC 60
 DB 1 ATGGAATTTTTCATTAATCTTGTGGCAGCCGCTGCTTTCGCTTCAAAATCCTTTGTT 60
 QY 61 GTCATCCCCAGAGAGAGGTCACGTTGTGAAAGGCTCGGGGCTTTCATCGCGCCCTG 120
 DB 61 GTCATCCCCAGAGAGGTCACGTTGTGAAAGGCTCGGGGCTTTCATCGCGCCCTG 120
 QY 121 ACGGCGGTTTGAATATTTTGTATTCCTTATTCAGACCGCTCGCTTACCGCAATTCGCTG 180
 DB 121 ACGGCGGTTTGAATATTTTGTATTCCTTATTCAGACCGCTCGCTTACCGCAATTCGCTG 180
 QY 181 AAGGAATCCCTTTAAGAGTACCCAGCCAGCTGTGATCAGCGGCGAATTAAGCAATTG 240
 DB 181 AAGGAATCCCTTTAAGAGTACCCAGCCAGCTGTGATCAGCGGCGAATTAAGCAATTG 240
 QY 241 ACTGTGACGGGATCATCTATTTTCCAAAGTAAACGATCCCAACTCGCTCATACGGTTG 300
 DB 241 ACTGTGACGGGATCATCTATTTTCCAAAGTAAACGATCCCAACTCGCTCATACGGTTG 300
 QY 301 AGCAACTACATTAATGCAATTAACCAAGCTTGCCCAACGACGCTGCGTTTCGTTATCGGG 360
 DB 301 AGCAACTACATTAATGCAATTAACCAAGCTTGCCCAACGACGCTGCGTTTCGTTATCGGG 360
 QY 361 CGTATGAGTTTGAACAAACGTTTGAAGAAACGACGCAAAATCAACGATACCGTCTTC 420

DB 361 CGTATGAGTTTGAACAAACGTTTGAAGAAACGACGCAAAATCAACGACGCTCTTC 420
 QY 421 GCCCTGATGAAGCCCGCGGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGAT 480
 DB 421 GCCCTGATGAAGCCCGCGGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGAT 480
 QY 481 TTGGTTCCGCGCAAGAAATCTTGGCGCAATGACGACCAAAATTAACCGCGACGCA 540
 DB 481 TTGGTTCCGCGCAAGAAATCTTGGCGCAATGACGACCAAAATTAACCGCGACGCA 540
 QY 541 AAACGCGCCGATTTGCGCAATCCGAAGCCGCTAAATTCGAACAAATCAACCTTGCA 600
 DB 541 AAACGCGCCGATTTGCGCAATCCGAAGCCGCTAAATTCGAACAAATCAACCTTGCA 600
 QY 601 GGTGACGCTGAAGCCGAATTCACATTCGAAGCGGCTCAGCTCGGTCAATGCG 660
 DB 601 GGTGACGCTGAAGCCGAATTCACATTCGAAGCGGCTCAGCTCGGTCAATGCG 660
 QY 661 TCCATATGCCAGAAATGCGCGCATCAACGCGGCAAGGCGAAGCGGATCCCTGCGC 720
 DB 661 TCCATATGCCAGAAATGCGCGCATCAACGCGGCAAGGCGAAGCGGATCCCTGCGC 720
 QY 721 CTGTGTCGGAAGCCGAATTCGCAATCCGTCAAATTCGCGCGCTTGAACCCAA 780
 DB 721 CTGTGTCGGAAGCCGAATTCGCAATCCGTCAAATTCGCGCGCTTGAACCCAA 780
 QY 781 GCGCGGCGGATGCGGTCATCTGAAGATTGCGGAACATTAATGACCGGCTTCAACAT 840
 DB 781 GCGCGGCGGATGCGGTCATCTGAAGATTGCGGAACATTAATGACCGGCTTCAACAT 840
 QY 841 CTTCGCAAGAAAGCAATTCGCTGATTATGATGCGCGCAATGTTGCGGACATCGGCGCTG 900
 DB 841 CTTCGCAAGAAAGCAATTCGCTGATTATGATGCGCGCAATGTTGCGGACATCGGCGCTG 900
 QY 901 ATTTCTGCGGATGAATTTATTCAGACGACGCAAAACCGCCAAATTA 948
 DB 901 ATTTCTGCGGATGAATTTATTCAGACGACGCAAAACCGCCAAATTA 948

RESULT 10
 AAA81268
 ID AAA81268 standard; DNA; 948 BP.

XX AAA81268;

XX 04-DEC-2000 (first entry)

DE N. meningitidis partial DNA sequence a519-1.seq SEQ ID NO:978.

XX *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KM *Meningococcus B*; MenB; de.

XX *Neisseria meningitidis*.

XX WO200022430-A2.

XX 20-APR-2000.

PF 08-OCT-1999; 99WO-US023573.

XX 09-OCT-1998; 98US-0103794P.

PR 30-APR-1999; 99US-0132068P.

XX (CHIR) CHIRON CORP.

XX Frazer CM, Hickey E, Peterson J, Tectelin H, Venter JC;
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scalato E;
 PI Rappuoli R, Pizsa M;
 XX
 DR WPI; 2000-318079/27.
 DR P-PSDB; AAB25628.

XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
PT in the diagnosis and treatment of *N. meningitidis* infection and other
PT *Neisseria* infections, for example, *N.gonorrhoea*.
XX

PS Claim 9, Page 74-75; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins
CC from *Neisseria* genomic sequences. AA81453 to AA82414 represent
CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
CC AA81260 to AA81303 and AA825620 to AA825663 represent *Neisseria* DNA
CC sequences and their corresponding proteins; AA81254 to AA81259 and
CC AA81304 to AA81321 represent PCR primers used in the isolation of
CC *Neisseria meningitidis* DNA sequences; and AA81322 to AA81452 represent
CC *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to *Neisseria* bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against *Meningococcus B*; against all serotypes; and/or against all
CC pathogenic *Neisseriae*. Identification of sequences from the *Bacterium*
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious *Meningococcus B*
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX

XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;

XX Query Match 93.9%; Score 890.4; DB 3; Length 948;

XX Best Local Similarity 96.2%; Pred. No. 1.3e-258;

XX Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```
QY 1 ATGGAATTTTTCATATCTTGTGGCAGCCGCTGCGCTTTTGGCTTCAAACTCTTGTG 60
DB 1 ATGGAATTTTTCATATCTTGTGGCAGCCGCTGCGCTTTTGGCTTCAAACTCTTGTG 60
QY 61 GTCAATCCCGCAGAGAGTTCAGCTTGTGCAAAAGCTGCGGCTTCATCGCCCTG 120
DB 61 GTCAATCCCGCAGAGAGTTCAGCTTGTGCAAAAGCTGCGGCTTCATCGCCCTG 120
QY 61 GTCAATCCCGCAGAGAGTTCAGCTTGTGCAAAAGCTGCGGCTTCATCGCCCTG 120
DB 61 GTCAATCCCGCAGAGAGTTCAGCTTGTGCAAAAGCTGCGGCTTCATCGCCCTG 120
QY 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGGCTGCGCTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGGCTGCGCTACCGCATTCGCTG 180
QY 181 AAAAGAAATCCCTTTAGACCTACCCAGCCGCTGTCATCAACCGGGAATTAATCGCAATTG 240
DB 181 AAAAGAAATCCCTTTAGACCTACCCAGCCGCTGTCATCAACCGGGAATTAATCGCAATTG 240
QY 181 AAAAGAAATCCCTTTAGACCTACCCAGCCGCTGTCATCAACCGGGAATTAATCGCAATTG 240
DB 181 AAAAGAAATCCCTTTAGACCTACCCAGCCGCTGTCATCAACCGGGAATTAATCGCAATTG 240
QY 241 ACTGTTGAGCGCATCATATTTTCCAGTAACCGAATCCCAACTGCGCTCATACGAGTTG 300
DB 241 ACTGTTGAGCGCATCATATTTTCCAGTAACCGAATCCCAACTGCGCTCATACGAGTTG 300
QY 241 ACTGTTGAGCGCATCATATTTTCCAGTAACCGAATCCCAACTGCGCTCATACGAGTTG 300
DB 241 ACTGTTGAGCGCATCATATTTTCCAGTAACCGAATCCCAACTGCGCTCATACGAGTTG 300
QY 301 AGCAACTACATTAATGCGCATTAACCGAGCTTGGCCAAAGACGCTGCTTCCGTTATCGGG 360
DB 301 AGCAACTACATTAATGCGCATTAACCGAGCTTGGCCAAAGACGCTGCTTCCGTTATCGGG 360
QY 361 CGTATGAGATTGGAACAAAGCTTTGAAGACCGGCAAGAAATCAACATGACCTGCTTCC 420
DB 361 CGTATGAGATTGGAACAAAGCTTTGAAGACCGGCAAGAAATCAACATGACCTGCTTCC 420
QY 361 CGTATGAGATTGGAACAAAGCTTTGAAGACCGGCAAGAAATCAACATGACCTGCTTCC 420
DB 361 CGTATGAGATTGGAACAAAGCTTTGAAGACCGGCAAGAAATCAACATGACCTGCTTCC 420
QY 421 GCCCTCGATGAAGCCGCGGAGCTTGGGGTGTGAAGGTTTTCGTTATGAGTTAAAGAC 480
DB 421 GCCCTCGATGAAGCCGCGGAGCTTGGGGTGTGAAGGTTTTCGTTATGAGTTAAAGAC 480
QY 481 TTGGTTCCGCGCAAGAAATCCTTGGCGAATGACGACCAATTAACGCGCAACGCGAA 540
DB 481 TTGGTTCCGCGCAAGAAATCCTTGGCGAATGACGACCAATTAACGCGCAACGCGAA 540
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DB 481 TTGGTTCCGCGCAAGAAATCCTTGGCTCAATGACGCGCAAAATTAAGTCTGAAACGCGAA 540
QY 541 AAAGCGCCGCTATTTGCGAATCCGAAGCCGTAATAATCGAAACAATCAACTTGGCAGT 600
DB 541 AAAGCGCCGCTATTTGCGAATCCGAAGCCGTAATAATCGAAACAATCAACTTGGCAGT 600
QY 601 GGTGAGCGTGAAGCCGAAATTCACAAATTCGAGGCGAAGCTCAGGCTGCGTCAATGCG 660
DB 601 GGTGAGCGTGAAGCCGAAATTCACAAATTCGAGGCGAAGCTCAGGCTGCGTCAATGCG 660
QY 601 GGTGAGCGTGAAGCCGAAATTCACAAATTCGAGGCGAAGCTCAGGCTGCGTCAATGCG 660
DB 601 GGTGAGCGTGAAGCCGAAATTCACAAATTCGAGGCGAAGCTCAGGCTGCGTCAATGCG 660
QY 661 TTCGAATGCGGAAATATGCGCCGATCAACCGCGCCAAAGCGGAAATCCCTGCGC 720
DB 661 TTCGAATGCGGAAATATGCGCCGATCAACCGCGCCAAAGCGGAAATCCCTGCGC 720
QY 721 CTTGTTGCGGAAAGCAATGCGGAGCCATCCGTAATAATGCGCGCCCTTCAAAACCAA 780
DB 721 CTTGTTGCGGAAAGCAATGCGGAGCCATCCGTAATAATGCGCGCCCTTCAAAACCAA 780
QY 781 GCGGCGGCGGATGCGGCTCAATCTGAAGATTGCGGAACAAATGTAAGCGGCTTCAACAT 840
DB 781 GCGGCGGCGGATGCGGCTCAATCTGAAGATTGCGGAACAAATGTAAGCGGCTTCAACAT 840
QY 841 CTTGCGCAAAAGAAAGCAATAGCTGATTAATGCGCGCCCAATGTTGCGCAATGCGGAGCCTG 900
DB 841 CTTGCGCAAAAGAAAGCAATAGCTGATTAATGCGCGCCCAATGTTGCGCAATGCGGAGCCTG 900
QY 901 ATTCTGCGGCGATGAATATTTATGACAGCAGCAAAACCGCAATTA 948
DB 901 ATTCTGCGGCGATGAATATTTATGACAGCAGCAAAACCGCAATTA 948
```

RESULT 11

AAA81265

ID AAA81265 standard; DNA; 948 BP.

XX AAA81265;

XX 04-DEC-2000 (first entry)

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Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
PT in the diagnosis and treatment of *N. meningitidis* infection and other
PT *Neisseria* infections, for example, *N.gonorrhoea*.
PS Claim 9, Page 72; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins
CC from *Neisseria* genomic sequences. AA81453 to AA82414 represent

CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used

XX Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;

Query Match 93.9%; Score 890.4; DB 3; Length 948;

Best Local Similarity 96.2%; Pred. No. 1.3e-258;

Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```

QY 1 ATGGAATTTTTCATATCTTGTGGCAGCCGCGCTTTCGCTTCAAAATCCTTTGTC 60
DB 1 ATGGAATTTTTCATATCTTGTGGCAGCCGCGCTTTCGCTTCAAAATCCTTTGTC 60
QY 61 GTGATCCCCCAGCAGAAAGTCCAGCTTGTGAAAAGCTCGGCTTTCATCGCCCTG 120
DB 61 GTGATCCCCCAGCAGAAAGTCCAGCTTGTGAAAAGCTCGGCTTTCATCGCCCTG 120
QY 121 ACGGCGGTTTGAATTTTGAATTCCTTATCGACCGGCTGCGCTACCGCATCGCGTG 180
DB 121 ACGGCGGTTTGAATTTTGAATTCCTTATCGACCGGCTGCGCTACCGCATCGCGTG 180
QY 181 AAGAAATCCCTTTAGACGTACCCAGCCAGCTCTGCATACCGCGCATATACGAAATG 240
DB 181 AAGAAATCCCTTTAGACGTACCCAGCCAGCTCTGCATACCGCGCATATACGAAATG 240
QY 241 ACTGTTGACGCGATCATTAATTCAGTAACCGATCCCAATCTGCTCATACGCTTGC 300
DB 241 ACTGTTGACGCGATCATTAATTCAGTAACCGATCCCAATCTGCTCATACGCTTGC 300
QY 301 AGCACTACATTAATGCGCATTTACCAAGTACCGACCCCAATCTGCTCATACGCTTGC 360
DB 301 AGCACTACATTAATGCGCATTTACCAAGTACCGACCCCAATCTGCTCATACGCTTGC 360
QY 361 CGTATGAGATTGAGCAAAAGCTTTGAGAAAGCGCAGCAAAATCAACAGTACCGCTTCC 420
DB 361 CGTATGAGATTGAGCAAAAGCTTTGAGAAAGCGCAGCAAAATCAACAGTACCGCTTCC 420
QY 421 GCCCTCGATGAAGCGCGCGGCGCTTGGGCTGTGAAAGTCTTCGTTACGAAATCAAGAT 480
DB 421 GCCCTCGATGAAGCGCGCGGCGCTTGGGCTGTGAAAGTCTTCGTTACGAAATCAAGAT 480
QY 481 TTGGTTCCCGCGCAAAATCTTGGCGGATGCGGCAAAATTAACCGCGCAAGCGCA 540
DB 481 TTGGTTCCCGCGCAAAATCTTGGCGGATGCGGCAAAATTAACCGCGCAAGCGCA 540
QY 541 AAACGGCGCCGATTTGCGCATCCGAAAGCGCTTAAATGCAACAATCAACCTTGCCAGT 600
DB 541 AAACGGCGCCGATTTGCGCATCCGAAAGCGCTTAAATGCAACAATCAACCTTGCCAGT 600
QY 601 GGTGACGCGTGAAGCGCGAAATCCCAACATTCGAAAGGAGGCTCAAGGCTCGGTCATGCG 660
DB 601 GGTGACGCGTGAAGCGCGAAATCCCAACATTCGAAAGGAGGCTCAAGGCTCGGTCATGCG 660
QY 661 TCCAAATGCGGAAATGCGCGCGCATCAACCGCGCAAAAGGAGGCAATCCCTTGCGC 720
DB 661 TCCAAATGCGGAAATGCGCGCGCATCAACCGCGCAAAAGGAGGCAATCCCTTGCGC 720
QY 721 CTGTTGCGGAAAGCGCAATGCGCGCATCAACCGCGCAAAAGGAGGCAATCCCTTGCGC 780
DB 721 CTGTTGCGGAAAGCGCAATGCGCGCATCAACCGCGCAAAAGGAGGCAATCCCTTGCGC 780
QY 781 GCGCGGCGCGATGCGGTCAATCTGAAGATGCGGCAACATTAAGTACCGCGCTTCAACAT 840
DB 781 GCGCGGCGCGATGCGGTCAATCTGAAGATGCGGCAACATTAAGTACCGCGCTTCAACAT 840

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QY 841 CTTGCCAAAGAAAGCAATACGCTGATTATGCCCCCAATGTTGCCGACATCGAGCGCTG 900
DB 841 CTTGCCAAAGAAAGCAATACGCTGATTATGCCCCCAATGTTGCCGACATCGAGCGCTG 900
QY 901 ATTTCTGCGCGCATGAAATTAATATGACAGCAGCAAAACCGCAATTA 948
DB 901 ATTTCTGCGCGCATGAAATTAATATGACAGCAGCAAAACCGCAATTA 948

```

RESULT 13

AAFP2150

AAFP2150 standard; DNA; 948 BP.

AAFP2150;

13-MAR-2001 (first entry)

N. meningitidis partial DNA sequence as19.seq SEQ ID NO:12.

Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;

diagnosis; antigen; detection; infection; gene therapy; antibacterial;

ds.

Neisseria meningitidis.

MO20006791-A1.

08-MAR-2000; 2000WO-US005928.

30-APR-1999; 99US-0132068P.

08-OCT-1999; 99WO-US023573.

28-FEB-2000; 2000GB-00004695.

(CHIR) CHIRON CORP.

(GENO-) INST GENOMIC RES.

Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;

Maignani V, Galeotti C, Mora M, Racci G, Scarselli M, Scarlato V;

Rappuoli R, Frazer CM, Grandi G;

WPI; 2000-647603/62.

P-PsDB; AAB58555.

Neisseria meningitidis B full length genome sequence and open reading

frames are used to detect, treat and prevent Neisserial infections.

Example 1; Page 73; 692pp; English.

The present invention describes the full length genome of Neisseria

meningitidis B (NMB). The sequences in AAFP21544 and AAFP21607 to AAFP21613

represent fragments of the NMB genomic sequence, as the sequence was too

long to go in a record on its own it was split into 8 sequences which

overlap each other at the beginning and end of each sequence by 49980 bp

(i.e. the last 49980 bp of AAFP21544 is repeated at the beginning of

AAFP21607, the last 49980 bp of AAFP21607 are repeated at the beginning of

AAFP21608, and so on). AAFP21545 to AAFP21588 encode the Neisseria proteins

given in AAB58550 to AAB58593, and AAFP21589 to AAFP21606 represent PCR

primers which are used in the exemplification of the present invention.

The NMB genome and fragments from it have antibacterial activity, and can

be used in vaccines and gene therapy. Neisseria nucleic acids, proteins

and/or antibodies which binds to the proteins can be used in compositions

for treating or preventing infection due to Neisserial bacteria or as a

diagnostic reagent for detecting the presence of Neisserial bacteria or

of antibodies raised to Neisserial bacteria. Computers, computer memory,

computer storage medium or computer databases can be used in a search to

identify open reading frames (ORFs) or coding sequences within the NMB

genome. The DNA sequences provide further opportunities to find antigenic

or immunogenic proteins which are more effective in vaccines than the

outer membrane proteins currently used

Sequence 948 BP; 244 A; 270 C; 227 G; 207 T; 0 U; 0 Other;

Query Match 93.9%; Score 890.4; DB 3; Length 948;
Best Local Similarity 96.2%; Pred. No. 1.3e-258;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```

OY 1 ATGGAATTTTTCATATCTGTGTGGCAGCCGTCGCGCTTTTCGCTTCAAAATCCTTTGTC 60
DB 1 ATGGAATTTTTCATATCTGTGTGGCAGCCGTCGCGCTTTTCGCTTCAAAATCCTTTGTC 60
OY 61 GTCAATCCCAAGCAGAGAGTCCACGTTGTGCAAAAGCTCGGGCGTTTCATCGCCCTG 120
DB 61 GTCAATCCCAAGCAGAGAGTCCACGTTGTGCAAAAGCTCGGGCGTTTCATCGCCCTG 120
OY 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGGTCGCTTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGGTCGCTTACCGCATTCGCTG 180
OY 181 AAAAATATCCCTTTAGAGTACCCGACGAGTCTGCATCAACGCGGATTAATCGCAATTG 240
DB 181 AAAAATATCCCTTTAGAGTACCCGACGAGTCTGCATCAACGCGGATTAATCGCAATTG 240
OY 241 ACTGTGACGGGATCATCTATTTCCAGTAACCGATCCCAAACTGCGCTCATACGCTTCG 300
DB 241 ACTGTGACGGGATCATCTATTTCCAGTAACCGATCCCAAACTGCGCTCATACGCTTCG 300
OY 301 AGCACTACATTTATGGCAATTAACCGAGCTTGGCCAAACGACGCTGCTTTCGTTATCGGG 360
DB 301 AGCACTACATTTATGGCAATTAACCGAGCTTGGCCAAACGACGCTGCTTTCGTTATCGGG 360
OY 361 CGTATGAGTTTGAACAAACGTTTGAAGAACCGGACGCAAAATCAAGTACCGTCTCC 420
DB 361 CGTATGAGTTTGAACAAACGTTTGAAGAACCGGACGCAAAATCAAGTACCGTCTCC 420
OY 421 GCCCTCGATGAAAGCCGCGGGCTTGGGGTGTGAAGTCTCCGTTTACCAATCAAGAT 480
DB 421 GCCCTCGATGAAAGCCGCGGGCTTGGGGTGTGAAGTCTCCGTTTACCAATCAAGAT 480
OY 481 TTGTTCCGCGCAGAAATCCCTTCGCGCAATGACGACCAAAATTAACGCGCAACGCGAA 540
DB 481 TTGTTCCGCGCAGAAATCCCTTCGCGCAATGACGACCAAAATTAACGCGCAACGCGAA 540
OY 541 AAAACGCGCCGTTATGCGCAATCCGAGGCGCTTAATTAATGAACCAATCACTTGCAGT 600
DB 541 AAAACGCGCCGTTATGCGCAATCCGAGGCGCTTAATTAATGAACCAATCACTTGCAGT 600
OY 601 GGTGACGCGTGAAGCCGGAATCCCAATCCGAAAGGAGGCTCAGGCTGCGGTCAATGCG 660
DB 601 GGTGACGCGTGAAGCCGGAATCCCAATCCGAAAGGAGGCTCAGGCTGCGGTCAATGCG 660
OY 661 TCCAAATGCGAAGAAATCGCCGCAATCAACGCGCAAAAGCGGATCCCTGCGC 720
DB 661 TCCAAATGCGAAGAAATCGCCGCAATCAACGCGCAAAAGCGGATCCCTGCGC 720
OY 721 CTGTGTTGCGAAGCAATCGCAAGCCATCCGTCAATTTGCGCGCGCTTCAACCCAA 780
DB 721 CTGTGTTGCGAAGCAATCGCAAGCCATCCGTCAATTTGCGCGCGCTTCAACCCAA 780
OY 781 GCGCGGCGGATGCGGTCAATCTGAAGATTTGGGGAACATAGCTAGCCCGCTTCAACAT 840
DB 781 GCGCGGCGGATGCGGTCAATCTGAAGATTTGGGGAACATAGCTAGCCCGCTTCAACAT 840
OY 841 CTGTCGAAGAAAGCAATACGCTGATTTATGCGCGCAATGTTTCCGACATCGGACGCTG 900
DB 841 CTGTCGAAGAAAGCAATACGCTGATTTATGCGCGCAATGTTTCCGACATCGGACGCTG 900
OY 901 ATTTCTGCGCGATGAATTAATTCAGACAGCAAGCAAAACCGCCAAATTA 948
DB 901 ATTTCTGCGCGATGAATTAATTCAGACAGCAAGCAAAACCGCCAAATTA 948

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RESULT 14
AA254581

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ID AA254581 standard; DNA; 951 BP.
XX
AC AA254581;
XX
DT 15-SEP-2003 (revised)
DT 21-MAR-2000 (first entry)
DE Neisseria gonorrhoeae ORF 519 partial DNA sequence SEQ ID NO:3047.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy; ds.
OS
XX Neisseria gonorrhoeae.
XX
FN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0098962P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (GENR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Frazer C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR P-PSDB; AAY75779.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Example 1; Page 74; 1453bp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides which may themselves have also be
CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 951 BP; 252 A; 274 C; 228 G; 197 T; 0 U; 0 Other;

```

Query Match 93.5%; Score 886.6; DB 3; Length 951;
Best Local Similarity 96.7%; Pred. No. 1.9e-257;
Matches 916; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

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OY 1 ATGGAATTTTTCATATCTGTGTGGCAGCCGTCGCGCTTTTCGCTTCAAAATCCTTTGTC 60
DB 1 ATGGAATTTTTCATATCTGTGTGGCAGCCGTCGCGCTTTTCGCTTCAAAATCCTTTGTC 60
OY 61 GTCAATCCCAAGCAGAGAGTCCACGTTGTGCAAAAGCTCGGGCGTTTCATCGCCCTG 120
DB 61 GTCAATCCCAAGCAGAGAGTCCACGTTGTGCAAAAGCTCGGGCGTTTCATCGCCCTG 120

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Qy 121 ACGCCGGTTGAATATTTGATTCCTTTATCGACCGCGTCGCGCTACCGGCATTCGCTG 180
Db 121 ACGCCGGTTGAATATTTGATTCCTTTATCGACCGCGTCGCGCTACCGGCATTCGCTG 180
Qy 181 AAAAATATCCCTTTAGAGATACCGACGAGCTTTCATCAAGCGCGATTAATACCAATTG 240
Db 181 AAAAATATCCCTTTAGAGATACCGACGAGCTTTCATCAAGCGCGATTAATACCAATTG 240
Qy 241 ACTGTGACGCGCATCATTTATTTCCAAAGTAACCGATCCCAACTGCGCTCATACGATTCG 300
Db 241 ACTGTGACGCGCATCATTTATTTCCAAAGTAACCGATCCCAACTGCGCTCATACGATTCG 300
Qy 301 AGCAATACATTTATGGAATTAACCGAGCTTCCCAAGAGCGCTGCGTTCCGTTATCGGG 360
Db 301 AGCAATACATTTATGGAATTAACCGAGCTTCCCAAGAGCGCTGCGTTCCGTTATCGGG 360
Qy 361 CGTATGAGTTGAGCAAAAAGCTTTGAGAGACGCGACCAATCAACAGTACCGTCTCC 420
Db 361 CGTATGAGTTGAGCAAAAAGCTTTGAGAGACGCGACCAATCAACAGTACCGTCTCC 420
Qy 421 GCCCTCGATGAAAGCGCGGGGGCTTGGGGTGTGAAGCTCCGTTACGAATCAAGGAT 480
Db 421 GCCCTCGATGAAAGCGCGGGGGCTTGGGGTGTGAAGCTCCGTTACGAATCAAGGAT 480
Qy 481 TTGGTTCCGCGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTAACCGCGAAACGCGAA 540
Db 481 TTGGTTCCGCGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTAACCGCGAAACGCGAA 540
Qy 541 AAAGCGCGCGTATTTGCCGAATCCGAAAGCGGTAAATCGAACAAATCAACTCTTGCCAGT 600
Db 541 AAAGCGCGCGTATTTGCCGAATCCGAAAGCGGTAAATCGAACAAATCAACTCTTGCCAGT 600
Qy 601 GGTGAGGTGAAAGCGGAATCCAAATCGAAGCGCGGTCAAGGCTGCGGTCAATGCG 660
Db 601 GGTGAGGTGAAAGCGGAATCCAAATCGAAGCGCGGTCAAGGCTGCGGTCAATGCG 660
Qy 661 TCCATGCGCGCAAGAAATCGCCGATCAACCGCGCAAGCGCAAGCGGAATCCCTGCGC 720
Db 661 TCCATGCGCGCAAGAAATCGCCGATCAACCGCGCAAGCGCAAGCGGAATCCCTGCGC 720
Qy 721 CTTGTGCGCAAGCAATCGCGAAGCCATCCGTCAATTTGCGCGCGCTTCAAAACCAA 780
Db 721 CTTGTGCGCAAGCAATCGCGAAGCCATCCGTCAATTTGCGCGCGCTTCAAAACCAA 780
Qy 781 GCGCGGGGAGTGTGCTCAATCTGAAGTTGCGGAATCGTAACCGCGCTTCAACAT 840
Db 781 GCGCGGGGAGTGTGCTCAATCTGAAGTTGCGGAATCGTAACCGCGCTTCAACAT 840
Qy 841 CTTGCGCAAGAAAGCAATACGCTGATTTAGCCGCGCAATGTTGCGCATCGGACGCTG 900
Db 841 CTTGCGCAAGAAAGCAATACGCTGATTTAGCCGCGCAATGTTGCGCATCGGACGCTG 900
Qy 901 A-TTTTGTGCGGATGAAAATTTATCGACAGACGCAAAACCGCCAAA 945
Db 901 AATTTTGTGCGGATGAAAATTTTTCGCGCAGAGCAAAACGCGCAA 947

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RESULT 15
 ID AAA81264 standard; DNA; 951 BP.

XX AAA81264;

XX 15-SEP-2003 (revised)
 DT 04-DEC-2000 (first entry)

XX N. gonorrhoeae partial DNA sequence g519.seq SEQ ID NO:970.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KM Meningococcus B; Memb; ds.

XX

OS Neisseria gonorrhoeae.
 XX WO200022430-A2.
 XX 20-APR-2000.
 XX 08-OCT-1999; 99WO-US023573.
 XX 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX (CHIR) CHIRON CORP.
 XX Frazer CM, Hickey E, Peterson J, Tetzelin H, Venter JC,
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
 PI Rappuoli R, Pizzo M,
 XX WPI; 2000-318079/27.
 DR P-PSDB; AAB25624.
 XX
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 XX
 PS Claim 9; Page 71; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81460 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis Memb polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition against them, can be used as a medicament (or in the manufacture of a medicament) for treating, for preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions. (Updated on 15-SEP-2003 to standardise OS field)

Sequence 951 BP; 252 A; 274 C; 228 G; 197 T; 0 U; 0 Other;

Query Match 93.5%; Score 886.6; DB 3; Length 951;

Best Local Similarity 96.7%; Pred. No. 1.9e-287;

Matches 916; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

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Qy 1 ATGGAATTTTTCATTTATCTTGTGGACAGCGGTGCGGCTTTTGGCTTCAAAATCCTTTGTC 60
Db 1 ATGGAATTTTTCATTTATCTTGTGGACAGCGGTGCGGCTTTTGGCTTCAAAATCCTTTGTC 60
Qy 61 GTCAATCCCGCAGCAAGAAAGTCAAGTGTGAAAAGGCTCGGGGCTTTCATCGGCGCTG 120
Db 61 GTCAATCCCGCAGCAAGAAAGTCAAGTGTGAAAAGGCTCGGGGCTTTCATCGGCGCTG 120
Qy 121 ACGGCGGTTTGAATATTTGATTCCTTTATCGACCGGCTGCGCTACCGCATTCGCTG 180
Db 121 ACGGCGGTTTGAATATTTGATTCCTTTATCGACCGGCTGCGCTACCGCATTCGCTG 180
Qy 181 AAAGAAATCCCTTTAGACGTAACCGACGAGTGTGATCAACGCGCATTAATACCAATTG 240
Db 181 AAAGAAATCCCTTTAGACGTAACCGACGAGTGTGATCAACGCGCATTAATACCAATTG 240

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Qy 241 ACTGTTGAGCGCATCATTTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTCG 300
Db 241 ACTGTTGAGCGCATCATTTTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTCG 300
Qy 301 AGCAACTCATTAATGAGCAATTAACCGATCCCAAACTGCGCTCATACGCTTCG 360
Db 301 AGCAACTCATTAATGAGCAATTAACCGATCCCAAACTGCGCTCATACGCTTCG 360
Qy 361 CGTATGAGCTTGAGCAAAAGCTTTGAGAGAGCGGCAAGATCAACAGTACGCTTCG 420
Db 361 CGTATGAGCTTGAGCAAAAGCTTTGAGAGAGCGGCAAGATCAACAGTACGCTTCG 420
Qy 421 GCCCTCGATGAGAGCGCGCGGCTTGGGGGTGGAAGCTCTCGTTAGCAATCAAGAT 480
Db 421 GCCCTCGATGAGAGCGCGCGGCTTGGGGGTGGAAGCTCTCGTTAGCAATCAAGAT 480
Qy 481 TTGTTTCCGCGCGCAAGAAATCCTTGGCGCAATGAGGCAAAATTAACGCGGAGCGGA 540
Db 481 TTGTTTCCGCGCGCAAGAAATCCTTGGCGCAATGAGGCAAAATTAACGCGGAGCGGA 540
Qy 541 AAACGCGCGCGTATGCGCAATCCGAGAGCGCTAAATTCGAACAATCAACCTTCAGT 600
Db 541 AAACGCGCGCGTATGCGCAATCCGAGAGCGCTAAATTCGAACAATCAACCTTCAGT 600
Qy 601 GGTGAGCTGAGAGCGCAATCCGAGAGCGCTCAAGGCTGAGGCTGAGGCTCAATGCG 660
Db 601 GGTGAGCTGAGAGCGCAATCCGAGAGCGCTCAAGGCTGAGGCTGAGGCTCAATGCG 660
Qy 661 TTCCATGCGCGAGAAATGCGCGCGCATCAACCGCGCAAGAGGAGGAGATCCGTGCGC 720
Db 661 TTCCATGCGCGAGAAATGCGCGCGCATCAACCGCGCAAGAGGAGGAGATCCGTGCGC 720
Qy 721 CTGTTGCGCAAGCAATGCGCAATCCGATCCGTAATTCGCGCGCTTCAAAACCA 780
Db 721 CTGTTGCGCAAGCAATGCGCAATCCGATCCGTAATTCGCGCGCTTCAAAACCA 780
Qy 781 GCGCGGCGCGATGCGCTCAATGGAAGTTGGGGAACAATAGTACGCGCTTCAACAT 840
Db 781 GCGCGGCGCGATGCGCTCAATGGAAGTTGGGGAACAATAGTACGCGCTTCAACAT 840
Qy 841 CTGTCGCAAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGACATCGGACGCTG 900
Db 841 CTGTCGCAAAAGCAATACGCTGATTAATGCGCGCAATGTTGCGGACATCGGACGCTG 900
Qy 901 A-TTTCGCGCGGATGAAATTTATGACAGAGCAAAACGCGCAAA 945
Db 901 A-TTTCGCGCGGATGAAATTTATGACAGAGCAAAACGCGCAAA 945
Qy 945 A-TTTCGCGCGGATGAAATTTATGACAGAGCAAAACGCGCAAA 947
Db 945 A-TTTCGCGCGGATGAAATTTATGACAGAGCAAAACGCGCAAA 947

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PR 30-APR-1999; 99US-0132068P.
PR 08-OCT-1999; 99WO-US023573.
PR 28-FEB-2000; 2000GB-00004655.
PA (CHIR ) INST GENOMIC RES.
PA (GENO-) INST GENOMIC RES.
PI Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC,
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarbelli M, Scarlato V,
PI Rappuoli R, Frazer CM, Grandi G;
DR WPI; 2000-647603/62.
DR P-PSDB; AAB58554.
PT Neisseria meningitidis B full length genome sequence, and open reading
PT frames are used to detect, treat and prevent Neisserial infections.
XX
XX Example 1; Page 71-72; 692pp; English.
XX
CC The present invention describes the full length genome of Neisseria
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences which
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions
CC for treating or preventing infection due to Neisserial bacteria or as a
CC diagnostic reagent for detecting the presence of Neisserial bacteria or
CC of antibodies raised for detecting the presence of Neisserial bacteria.
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines than the
CC outer membrane proteins currently used. (Updated on 15-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 951 BP; 252 A; 274 C; 228 G; 197 T; 0 U; 0 Other;

```

Query Match 93.5%; Score 886.6; DB 3; Length 951;

Best Local Similarity 96.7%; Pred. No. 1.9e-257;

Matches 916; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

```

Qy 1 ATGGAATTTTTCATATCTGTTGCGACCGCGCGGTTTGGGCTTCAATCCTTTGTC 60
Db 1 ATGGAATTTTTCATATCTGTTGCGACCGCGCGGTTTGGGCTTCAATCCTTTGTC 60
Qy 61 GTGATCCCGCAGCAGAGTCCAGCTTGTGAAAGGCTGCGGCTTTCATGCGGCTTC 120
Db 61 GTGATCCCGCAGCAGAGTCCAGCTTGTGAAAGGCTGCGGCTTTCATGCGGCTTC 120
Qy 121 ACGGCGGTTGTAATTTTGAATTCCTTTATGACCGCGGTGCTTACCGCCATTGCGTG 180
Db 121 ACGGCGGTTGTAATTTTGAATTCCTTTATGACCGCGGTGCTTACCGCCATTGCGTG 180
Qy 181 AAGGAATTCCTTTAGAGTACCGCAGGCTGTCATCAACGCGGATTAATGCGAATTG 240
Db 181 AAGGAATTCCTTTAGAGTACCGCAGGCTGTCATCAACGCGGATTAATGCGAATTG 240
Qy 241 ACTGTTGAGCGGATCATCTATTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTGG 300
Db 241 ACTGTTGAGCGGATCATCTATTCCAAAGTAACCGATCCCAAACTGCGCTCATACGCTTGG 300
Qy 301 AGCAACTCATTAATGAGCAATTAACCGATCCCAAACTGCGCTCATACGCTTGG 360
Db 301 AGCAACTCATTAATGAGCAATTAACCGATCCCAAACTGCGCTCATACGCTTGG 360
Qy 361 CGTATGAGCTTGAGCAAAAGCTTTGAGAGAGCGGCAAGATCAACAGTACGCTTCGCTCC 420

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Db 361 CGTATGAGTTGACAAAGCTTTGAGAGACGCGACGAAATCAACAGTACGTCCTCC 420
Qy 421 GCCCTCATGAAAGCCCGCGGCGCTTGGGCTGTGAAAGTCTCCGTTACGAATCAAGAT 480
Db 421 GCCCTCATGAAAGCCCGCGGCGCTTGGGCTGTGAAAGTCTCCGTTACGAATCAAGAT 480
Qy 481 TTGGTCCGCGGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTACCGCGGAACGCGAA 540
Db 481 TTGGTCCGCGGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTACCGCGGAACGCGAA 540
Qy 541 AAACGCGCCGCTATTCGCGAATCCGAAGCCGTAATAATCGAAACAATCAACCTTCCAGT 600
Db 541 AAACGCGCCGCTATTCGCGAATCCGAAGCCGTAATAATCGAAACAATCAACCTTCCAGT 600
Qy 601 GGTCAAGGTGAAGCCGGAATTCACCAATCCGAAGCCGAGCTTCAAGGCTGCGTAATGCG 660
Db 601 GGTCAAGGTGAAGCCGGAATTCACCAATCCGAAGCCGAGCTTCAAGGCTGCGTAATGCG 660
Qy 661 TCCAAATGCGGAAATCGCCGCGATCAACGCGCAAAAGCGGAAGCGAATCCCTGCGC 720
Db 661 TCCAAATGCGGAAATCGCCGCGATCAACGCGCAAAAGCGGAAGCGAATCCCTGCGC 720
Qy 721 CTTGTGCGGAGCCGAATGCGGAGCCATCCGTCAAATTCGCGCGCTTCAAAACCGAA 780
Db 721 CTTGTGCGGAGCCGAATGCGGAGCCATCCGTCAAATTCGCGCGCTTCAAAACCGAA 780
Qy 781 GCGCGGCGGATGCGGTCATCTGAAGATTCGCGAACAATCGTAGCGGCTTCAACAT 840
Db 781 AGCGGGGCGGATGCGGTCATCTGAAGATTCGCGAACAATCGTAGCGGCTTCAAAAT 840
Qy 841 CTTGCCAAGAAAGCAATACGCTGATTCGCGCGCAATGTTGCGGACATCGGACGCTG 900
Db 841 CTTGCCAAGAAAGCAATACGCTGATTCGCGCGCAATGTTGCGGACATCGGACGCTG 900
Qy 901 A-TTTCGCGCGCATGAAATTTATCGACAGCAAGAAACCGCGAA 945
Db 901 AATTTTCGCGCGCATGAAATTTTCGCGAGAGCAAAACCGCGCA 947

RESULT 17
AAZ53753
ID AAZ53753 standard; DNA, 948 BP.
XX
AC AAZ53753;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:1455.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
PN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
```

```
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M,
PI Peteren J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M,
PI Tettein H, Venter UC,
XX
DR WPI; 2000-062150/05.
DR P-PSDB; AAY74991.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 7; Page 779; 1453pp; English.
XX
AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
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Query Match 92.6%; Score 877.6; DB 3; Length 948;
Best Local Similarity 95.4%; Pred. No. 1e-254;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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Qy 1 ATGGAATTTTCAATATCTGTTGGCAGCGCGTTCGCTTTCGACTCAATCGCTTGTG 60
Db 1 ATGGAATTTTCAATATCTGTTGGTGAAGCGCGCTTCGCTTTCGACTCAATCGCTTGT 60
Qy 61 GTCAATCCCGCAGCAGAAAGTCAAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCCTG 120
Db 61 GTCAATCCCGCAGCAGAAAGTCAAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCCTG 120
Qy 121 ACGGCGGCTTGAATATTTGATTCCTTTATCGACCGCGCTTCGCTACCGCATTCGCTG 180
Db 121 ACGGCGGCTTGAATATTTGATTCCTTTATCGACCGCGCTTCGCTACCGCATTCGCTG 180
Qy 181 AAAGAAATCCCTTAGACGTACCCAGCAGGTGTCATCAAGCGGCAATATAGCAATG 240
Db 181 AAAGAAATCCCTTAGACGTACCCAGCAGGTGTCATCAAGCGGCAATATAGCAATG 240
Qy 241 ACTGTTAGCGGATCATCTATTTTCAGATTAACCGATCCCAACTCGGCTCATACGTTG 300
Db 241 ACTGTTAGCGGATCATCTATTTTCAGATTAACCGATCCCAACTCGGCTCATACGTTG 300
Qy 301 AGCAACTACATTAATGAGCAATTAACCGACTTCCCAAGCAAGCTGCTTCCGTTATG 360
Db 301 AGCAACTACATTAATGAGCAATTAACCGACTTCCCAAGCAAGCTGCTTCCGTTATG 360
Qy 361 CGTATGAGTTGACAAAGGTTGAAGAACGAGCAAGAAATCAACAGTACGTCCTCC 420
Db 361 CGTATGAGTTGACAAAGGTTGAAGAACGAGCAAGAAATCAACAGTACGTCCTCC 420
Qy 421 GCCCTCATGAAAGCCCGCGGCGCTTGGGCTGTGAAAGTCTCCGTTACGAATCAAGAT 480
Db 421 GCCCTCATGAAAGCCCGCGGCGCTTGGGCTGTGAAAGTCTCCGTTACGAATCAAGAT 480
Qy 481 TTGGTCCGCGGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTACCGCGGAACGCGAA 540
Db 481 TTGGTCCGCGGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTACCGCGGAACGCGAA 540
Qy 541 AAACGCGCCGCTATTCGCGAATCCGAAGCCGTAATAATCGAAACAATCAACCTTCCAGT 600
Db 541 AAACGCGCCGCTATTCGCGAATCCGAAGCCGTAATAATCGAAACAATCAACCTTCCAGT 600
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QY 601 GGTGACGCGGAGCCGGAATCCAAATCCGAGGCGAGGCTCAGGCTGCGGTCATGCG 660
DB 601 GGTGACGCGGAGCCGGAATCCAAATCCGAGGCGAGGCTCAGGCTGCGGTCATGCG 660
QY 661 TCCAAATGCGGAGAAATGCGCCGATCAACCGCGCCAAAGCGGAAATCCCTGCGC 720
DB 661 TCAAAATGCGGAGAAATGCGCCGATCAACCGCGCCAAAGCGGAAATCCCTGCGC 720
QY 721 CTTGTTGCGGAGAAATGCGGAGGCGATCCGTCATATGCGCGCCCTTCAAAACCA 780
DB 721 CTTGTTGCGGAGAAATGCGGAGGCGATCCGTCATATGCGCGCCCTTCAAAACCA 780
QY 781 GCGCGGCGGAGGCGGTCATCTGAAGATTGGGAAACAATAGTACCGGCTTCAACAT 840
DB 781 GCGCGGCGGAGGCGGTCATCTGAAGATTGGGAAACAATAGTACCGGCTTCAACAT 840
QY 841 CTTGCGCAAGAAAGCAATACGCTGATTATGCGCGCAATGTTGCCGACATCGGACGCTG 900
DB 841 CTTGCGCAAGAAAGCAATACGCTGATTATGCGCGCAATGTTGCCGACATCGGACGCTG 900
QY 901 ATTTCTGCGCGCATGAAATTTATCGACAGCGAAGAAACCGCAATAA 948
DB 901 ATTTCTGCGCGCATGAAATTTATCGACAGCGAAGAAACCGCAATAA 948
RESULT 18
AAZ54583
ID AAZ54583 standard; DNA; 948 BP.
AC AAZ54583;
XX 21-MAR-2000 (first entry)
DT
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:3051.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy; ds.
OS
OS Neisseria meningitidis.
XX
PN W09957280-A2.
XX 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
PR 25-FEB-1999; 99US-0121528P.
XX
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Frazer C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
PI Peterben U, Pizsa M, Rappoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelein H, Venter JC;
XX
XX WPI: 2000-062150/05.
DR P-PSDB; AAY75781.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
XX Example 1; Page 76; 1453pp; English.
XX
XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides

CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols
XX
SQ Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
Query Match 92.6%; Score 877.6; DB 3; Length 948;
Best Local Similarity 95.4%; Pred. No. 1e-254;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 ATGGAATTTTTCATATCTTGTGGCAGCGCGCGCTTTCGCTTCAATCTTGTG 60
DB 1 ATGGAATTTTTCATATCTTGTGGTACCGCGCGCTTTCGCTTCAATCTTGTG 60
QY 61 GTGATCCCCAGAGAGATCCAGCTGTGAAAGCTCGGCGTTTCATGCGCGCTG 120
DB 61 GTGATCCCCAGAGAGATCCAGCTGTGAAAGCTCGGCGTTTCATGCGCGCTG 120
QY 121 ACGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
DB 121 ACGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
QY 181 AAGAAATCCCTTTAGAGTACCGAGCGAGCTGATCAAGCGGATTAATAGCAATG 240
DB 181 AAGAAATCCCTTTAGAGTACCGAGCGAGCTGATCAAGCGGATTAATAGCAATG 240
QY 241 ACTGTTGACGCGCATCATATTTCCAAAGTAAACCGATCCCAATCGCTCATAGCGTTG 300
DB 241 ACTGTTGACGCGCATCATATTTCCAAAGTAAACCGATCCCAATCGCTCATAGCGTTG 300
QY 301 AGCAACTACATTTATGCGCAATTAACCAAGTGGCCCAAGAGCGCTTCCTTATCGGG 360
DB 301 AGCAACTACATTTATGCGCAATTAACCAAGTGGCCCAAGAGCGCTTCCTTATCGGG 360
QY 361 CGTATGAGTTGGAAGAAACGTTTGAAGAGCGAGAAATCAAGTACCGTCTCC 420
DB 361 CGTATGAGTTGGAAGAAACGTTTGAAGAGCGAGAAATCAAGTACCGTCTCC 420
QY 421 GCCCTGATGAAGCGCGCGGCTTGAGGTTGAAGTCTCTGTTACGAATCAAGAT 480
DB 421 GCCCTGATGAAGCGCGCGGCTTGAGGTTGAAGTCTCTGTTACGAATCAAGAT 480
QY 481 TTGTTTCCGCGCAAGAAATCTTGGCGCATGCGGCAAAATTAACCGCGAGCGAA 540
DB 481 TTGTTTCCGCGCAAGAAATCTTGGCGCATGCGGCAAAATTAACCGCGAGCGAA 540
QY 541 AAACGCGCGCGTATGCGGAAATCGAAGCGGTAATGAACAATCAACCTTGCAGT 600
DB 541 AAACGCGCGCGTATGCGGAAATCGAAGCGGTAATGAACAATCAACCTTGCAGT 600
QY 601 GGTGACGCGGAGCCGGAATCCAAATCCGAGGCGAGGCTCAGGCTGCGGTCATGCG 660
DB 601 GGTGACGCGGAGCCGGAATCCAAATCCGAGGCGAGGCTCAGGCTGCGGTCATGCG 660
QY 661 TCCAAATGCGGAGAAATGCGCCGATCAACCGCGCCAAAGCGGAAATCCCTGCGC 720
DB 661 TCAAAATGCGGAGAAATGCGCCGATCAACCGCGCCAAAGCGGAAATCCCTGCGC 720
QY 721 CTTGTTGCGGAGAAATGCGGAGGCGATCCGTCATATGCGCGCCCTTCAAAACCA 780
DB 721 CTTGTTGCGGAGAAATGCGGAGGCGATCCGTCATATGCGCGCCCTTCAAAACCA 780
QY 781 GCGCGGCGGAGGCGGTCATCTGAAGATTGGGAAACAATAGTACCGGCTTCAACAT 840
DB 781 GCGCGGCGGAGGCGGTCATCTGAAGATTGGGAAACAATAGTACCGGCTTCAACAT 840

QY 841 CTGCGCAAGAAAGCAATAGCCTGATTATGCGCGCAATGTTGCGACATCGAGCCTG 900
 CC |||||
 XX 841 CTGCGCAAGAAAGCAATAGCCTGATTATGCGCGCAATGTTGCGACATCGAGCCTG 900
 Db 841 CTGCGCAAGAAAGCAATAGCCTGATTATGCGCGCAATGTTGCGACATCGAGCCTG 900
 QY 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948
 CC |||||
 XX 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948
 Db 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948
 RESULT 19
 ID AAA81266 standard; DNA; 948 BP.
 XX AAA81266;
 AC
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE N. meningitidis partial DNA sequence m519-1.seq SEQ ID NO:974.
 XX
 KM Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KM antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KM Meningococcus B; MenB; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200022430-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US023573.
 XX
 PR 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC, Maignant V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappunio R, Pizza M;
 PI
 PI WPI; 2000-318079/27.
 DR P-PSDB; AAB25626.
 XX
 XX
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 PS
 PS Claim 9; Page 73; 1760pp; English.
 CC The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not

CC antigenically variable or at least more conserved than other more
 CC variable regions
 XX
 SO Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
 Query Match 92.6%; Score 877.6; DB 3; Length 948;
 Best Local Similarity 95.4%; Pred. No. 1e-254;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 1 ATGGAATTTTCTATCTGTTGGACGGCGGTTTTCGGCTCAATCCCTTGTG 60
 CC |||||
 Db 1 ATGGAATTTTCTATCTGTTGGACGGCGGTTTTCGGCTCAATCCCTTGTG 60
 QY 61 GTCAATCCCGCAGCAGAGAGTCAAGTGTGCAAAAGCTCGGGGCTTTCATCGGCCCTG 120
 CC |||||
 Db 61 GTCAATCCCGCAGCAGAGAGTCAAGTGTGCAAAAGCTCGGGGCTTTCATCGGCCCTG 120
 QY 121 ACGGCGGTTGAAATTTTGAATTCCTTTATCGACCGCGCTTCCGCGCATTCGCTG 180
 CC |||||
 Db 121 ACGGCGGTTGAAATTTTGAATTCCTTTATCGACCGCGCTTCCGCGCATTCGCTG 180
 QY 181 AAGAAATCCCTTAGAGGTAAGCCAGGCTGATCAAGCGCGGATTAAGCAATTA 240
 CC |||||
 Db 181 AAGAAATCCCTTAGAGGTAAGCCAGGCTGATCAAGCGCGGATTAAGCAATTA 240
 QY 241 ACTGTTGACGGCATCATCTATTTTCCAAAGTAACCGATCCAAACTCGCCTATACGTTTG 300
 CC |||||
 Db 241 ACTGTTGACGGCATCATCTATTTTCCAAAGTAACCGATCCAAACTCGCCTATACGTTTG 300
 QY 301 AGCAACTACATTAATGATGCAATTAACCGACTTCCCAACGACGCTGCTTCCGTTATCGG 360
 CC |||||
 Db 301 AGCAACTACATTAATGATGCAATTAACCGACTTCCCAACGACGCTGCTTCCGTTATCGG 360
 QY 361 CGTATGAGTTTGAACAAAGGTTTGAAGAACGCGACGAAATCAACAGTACGTCGTC 420
 CC |||||
 Db 361 CGTATGAGTTTGAACAAAGGTTTGAAGAACGCGACGAAATCAACAGTACGTCGTC 420
 QY 421 GCCCTCATGAGAGCGCGCGGCTTGGGATGTGAAGTCTCCGTTACGAATCAAGAT 480
 CC |||||
 Db 421 GCCCTCATGAGAGCGCGCGGCTTGGGATGTGAAGTCTCCGTTACGAATCAAGAT 480
 QY 481 TTGGTTCCGCGCAGAAATCTTTCGCGCAATGCGACACAAATTAACCGCGAA 540
 CC |||||
 Db 481 TTGGTTCCGCGCAGAAATCTTTCGCGCAATGCGACACAAATTAACCGCGAA 540
 QY 541 AAAGCGCCCGTATTTGCGCAATCCGAAGCGGTAAATTCGAACAAATCAACCTTGCCAGT 600
 CC |||||
 Db 541 AAAGCGCCCGTATTTGCGCAATCCGAAGCGGTAAATTCGAACAAATCAACCTTGCCAGT 600
 QY 601 GGTGAGGTAAGCGCGAAATCCAAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG 660
 CC |||||
 Db 601 GGTGAGGTAAGCGCGAAATCCAAATCCGAAGCGAGGCTCAGGCTGCGTCAATGCG 660
 QY 661 TCCAATGCGGAAATATCGCCCGCATCAACCGCGCAAGCGGAAATCCCTGCGC 720
 CC |||||
 Db 661 TCCAATGCGGAAATATCGCCCGCATCAACCGCGCAAGCGGAAATCCCTGCGC 720
 QY 721 CTGTTGCGGAAGCAATGCGCAATCCGATCCGTAATTCGCGCGCTTCAAAACCA 780
 CC |||||
 Db 721 CTGTTGCGGAAGCAATGCGCAATCCGATCCGTAATTCGCGCGCTTCAAAACCA 780
 QY 781 GGGCGGCGGATGCGGTCAATCTGAGATTGCGGACATTAAGTACGTCGCTTCAACAT 840
 CC |||||
 Db 781 GGGCGGCGGATGCGGTCAATCTGAGATTGCGGACATTAAGTACGTCGCTTCAACAT 840
 QY 841 CTGCGCAAGAAAGCAATAGCGTATTAATGCGCGCAATGTTGCGCATCGGAGCCTG 900
 CC |||||
 Db 841 CTGCGCAAGAAAGCAATAGCGTATTAATGCGCGCAATGTTGCGCATCGGAGCCTG 900
 QY 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948
 CC |||||
 Db 901 ATTTCTGCGCGCATGAAATTTATCGACGACGCAAAACCGCCAAATTA 948

RESULT 20
ID AAF21551 standard; DNA; 948 BP.
XX AAF21551;
AC AAF21551;
XX 13-MAR-2001 (first entry)
DT
XX N. meningitidis partial DNA sequence m519-1.seq SEQ ID NO:14.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
ds.
XX Neisseria meningitidis.
OS
XX WO200066791-A1.
XX
XX 09-NOV-2000.
XX
XX 08-MAR-2000; 2000MO-US005928.
XX
XX 30-APR-1999; 99US-0132068P.
PR 08-OCT-1999; 99MO-US023573.
PR 28-FEB-2000; 2000GB-00004695.
XX
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Pizza M, Hickey E, Peterson J, Tettelein H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Frazer CM, Grandi G;
XX
XX MPI: 2000-647603/62.
DR P-PEDB; AAB58556.
XX
PT Neisseria meningitidis B full length genome sequence and open reading
frames are used to detect, treat and prevent Neisserial infections.
XX
XX Example 1; Page 74; 692pp; English.
XX
XX The present invention describes the full length genome of Neisseria
meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
represent fragments of the NMB genomic sequence, as the sequence was too
long to go in a record on its own it was split into 8 sequences which
overlap each other at the beginning and end of each sequence by 49980 bp
(i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
primers which are used in the exemplification of the present invention.
XX The NMB genome and fragments from it have antibacterial activity, and can
be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
and/or antibodies which bind to the proteins can be used in compositions
for treating or preventing infection due to Neisserial bacteria or as a
diagnostic reagent for detecting the presence of Neisserial bacteria or
of antibodies raised to Neisserial bacteria. Computers, computer memory,
computer storage medium or computer databases can be used in a search to
identify open reading frames (ORFs) or coding sequences within the NMB
genome. The DNA sequences provide further opportunities to find antigenic
or immunogenic proteins which are more effective in vaccines than the
outer membrane proteins currently used
XX
XX Sequence 948 BP; 242 A; 261 C; 234 G; 211 T; 0 U; 0 Other;
SQ

Query Match 92.6%; Score 877.6; DB 3; Length 948;
Best Local Similarity 95.4%; Pred. No. 1e-254;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1 ATCGAATTTTCTTCTTCTTGGAGCGCGCGTTCGGCTTCAAAATCTTGTTC 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 ATGGAATTTTCTTCTTCTTGGAGCGCGCGTTCGGCTTCAAAATCTTGTTC 60
QY 61 GTCAATCCCCCAGCAGGAAGTCCAGCTTGTCGAAAGGCTCGGAGCTTTCATCGGCGCTG 120
DB 61 GTCAATCCACAAAGAGAGTCCAGCTTTCGAAAGGCTGGAGGCTTTCATCGGCGCTG 120
QY 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACGCGGTTCGCTTACCGCATTCGCTG 180
DB 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACGCGGTTCGCTTACCGCATTCGCTG 180
QY 181 AAAGAAATCCCTTTAGACGTACCCAGCGAGGTTCGATCAGCGCGGATTAATAGCAATTG 240
DB 181 AAAGAAATCCCTTTAGACGTACCCAGCGAGGTTCGATCAGCGCGGATTAATAGCAATTG 240
QY 241 ACTGTGACGGCATCATCTATTTCCAAAGTAAACGATCCCAACTGCGCTCATACGCTTCG 300
DB 241 ACTGTGACGGCATCATCTATTTCCAAAGTAAACGATCCCAACTGCGCTCATACGCTTCG 300
QY 301 AGCAACTACATTATGGAATTAACCAAGCTTGCCCAACGACGCTGCTTCGTTATCGG 360
DB 301 AGCAACTACATTATGGAATTAACCAAGCTTGCCCAACGACGCTGCTTCGTTATCGG 360
QY 361 CGTATGAGTTGACAAACGTTTGAAGACGCGACGAATCAAGTACGTCGTCTCC 420
DB 361 CGTATGAGTTGACAAACGTTTGAAGACGCGACGAATCAAGTACGTCGTCTTCG 420
QY 421 GCCCTGATGAAAGCGCGCGGCTTGCGGTGTAAGTCCCTCGTTAGAAATCAAGAT 480
DB 421 GCTTTGACGAGGCGCGCGGCTTGCGGTGTAAGTCCCTCGTTAGAAATCAAGAT 480
QY 481 TTGGTTCCGCGCAAGAAATCCTTCGCGCAATGACGAGCAAAATTAACGCGCAACGCGAA 540
DB 481 TTGGTTCCGCGCAAGAAATCCTTCGCGCAATGACGAGGCAAAATTAACGCGCAACGCGAA 540
QY 541 AAAGCGCGCGGTATTCGCAATTCGAGGCGCTTAATTCGAACAATCAACTTGCCTAGT 600
DB 541 AAAGCGCGCGGTATTCGCGCAATTCGAGGCGCTTAATTCGAACAATCAACTTGCCTAGT 600
QY 601 GGTGACGCGTGAAGCGGAAATCCAAATCCGAAAGGCGAGGCTCAGGCTGCGTCAATGCG 660
DB 601 GGTGACGCGTGAAGCGGAAATCCAAATCCGAAAGGCGAGGCTCAGGCTGCGTCAATGCG 660
QY 661 TCCAAATGCGAGAAATCGCCGCGCATCAACGCGCAAGGCGAAGCGGAATCCCTGCGC 720
DB 661 TCCAAATGCGAGAAATCGCCGCGCATCAACGCGCGCAAGGCGAAGCGGAATCCCTGCGC 720
QY 721 CTTGTTGCGAAGCCAAATGCGCAATTCGTCAAATTTGCCGCGCTTCAAAACCGAA 780
DB 721 CTTGTTGCGAAGCCAAATGCGCAATTCGTCAAATTTGCCGCGCTTCAAAACCGAA 780
QY 781 GCGCGGCGCGATGCGGTCAATTCGAAGATTCGGGAAACAATAGTACCGCGCTCAACAT 840
DB 781 GCGCGGCGCGATGCGGTCAATTCGAAGATTCGGGAAACAATAGTACCGCGCTCAACAT 840
QY 841 CTTGCAAGAAAGAAATGCGGTATGATGCGCGCAATGTTGCGGACATCGGACGCTG 900
DB 841 CTTGCAAGAAAGAAATGCGGTATGATGCGCGCAATGTTGCGGACATCGGACGCTG 900
QY 901 ATTTCGCGCGCATGAAATTTATGACAGACGACAAACCGCGCAATTA 948
DB 901 ATTTCGCGCGCATGAAATTTATGACAGACGACAAACCGCGCAATTA 948
RESULT 21
ID AAA81459 standard; DNA; 56609 BP.
XX
XX AAA81459;
AC
XX 04-DEC-2000 (first entry)
DT
XX N. meningitidis partial DNA sequence gnm_7 SEQ ID NO:7.
DB Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;

KM antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KM Meningococcus B; Memb; ds.
 XX Neisseria meningitidis.
 OS WO200022430-A2.
 XX 20-APR-2000.
 XX PD 08-OCT-1999; 99WO-US023573.
 XX PR 09-OCT-1998; 98US-0103794P.
 XX PR 30-APR-1999; 99US-0132068P.
 XX (CHIR) CHIRON CORP.
 PA Frazer CM, Hickey E, Peterson J, Tettein H, Venter JC,
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
 PI Rappuoli R, Pizzo M;
 XX WPI; 2000-318079/27.
 DR
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 PS Claim 7; Page 303-320; 1760dp; English.
 XX
 CC The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAA81460 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
 CC Neisseria meningitidis Memb polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions
 XX
 SQ Sequence 56609 BP; 14040 A; 15839 C; 14415 G; 12313 T; 0 U; 2 Other;
 Query Match 92.6%; Score 877.6; DB 3; Length 56609;
 Best Local Similarity 95.4%; Pred. No. 6.5e-25;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 1 ATGGAATTTTCATTATCTTGTGGACGCGTTCGCGTTTCGAGTCAAAATCCTTTGTC 60
 DB 684 ATGGAATTTTCATTATCTTGTGGTACCGTTCGCGTTTCGAGTCAAAATCCTTTGTT 743
 QY 61 GTCAATCCCGACGAGAGTCCAGTTCGAAAGGCTCGGCGTTTCATTCGCGCCCTG 120
 DB 744 GTCAATCCCGACGAGAGTCCAGTTCGAAAGGCTCGGCGTTTCATTCGCGCCCTG 803
 QY 121 ACGGCGGTTTGATTTGATTCCTTTATCGACGCGTTCGCTACCGCATTCGCTG 180
 DB 804 ACGGCGGTTTGATTTGATTCCTTTATCGACGCGTTCGCTACCGCATTCGCTG 863
 QY 181 AAAAATATCCCTTAGACGTACCGACGAGTCTGCATCAAGCGGATATATACCAATTG 240

DB 864 AAAAATATCCCTTAGACGTACCGACGAGTCTGCATCAAGCGGCAATATCCACCTG 923
 QY 241 ACTGTGACGGGCATCATCTATTTTCAGAGTAACGATCCGAAATCGGCTCATACGTTG 300
 DB 924 ACTGTGACGGGCATCATCTATTTTCAGAGTAACGATCCGAAATCGGCTCATACGTTG 983
 QY 301 AGCAATACATTTATGGAATTAACCCAGCTTGCCTCAAGAGAGAGAGAGAGAGAGAG 360
 DB 984 AGCAATACATTTATGGAATTAACCCAGCTTGCCTCAAGAGAGAGAGAGAGAGAGAG 1043
 QY 361 CGTATGAGTTTGACAAAGGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 1044 CGTATGAGTTTGACAAAGGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
 QY 421 GCCTCGATGAG 480
 DB 1104 GCTTTGACAG 1163
 QY 481 TTGGTTCCGCGCAAGAAATCTTCGCGCAATGCGAGCACAATTAACGCGGAA 540
 DB 1164 TTGGTTCCGCGCAAGAAATCTTCGCGCAATGCGAGCACAATTAACGCGGAA 1223
 QY 541 AAACGCGCGGTATTCGCGAATCCGAGAGCGGTAAATTCGAACAATCACTTGCAGT 600
 DB 1224 AAACGCGCGGTATTCGCGAATCCGAGAGCGGTAAATTCGAACAATCACTTGCAGT 1283
 QY 601 GGTAGGTTGAAGCGGAAATTCGAACAATTCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 1284 GGTAGGTTGAAGCGGAAATTCGAACAATTCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1343
 QY 661 TCCAAATCCGAGAAATTCGCGCGCATCAACCGCGCAAGAGAGAGAGAGAGAGAGAGAG 720
 DB 1344 TCCAAATCCGAGAAATTCGCGCGCATCAACCGCGCAAGAGAGAGAGAGAGAGAGAGAG 1403
 QY 721 CTTGTTCCGAGAGCAATTCGCGAAGCATTCGTAATTTGCGCGGCTTCAAAACCA 780
 DB 1404 CTTGTTCCGAGAGCAATTCGCGAAGCATTCGTAATTTGCGCGGCTTCAAAACCA 1463
 QY 781 GCGCGGCGAGATGCGGCAATTCGAAGATTGCGGCAATTCGAGCGGCTTCAACAT 840
 DB 1464 GCGCGGCGAGATGCGGCAATTCGAAGATTGCGGCAATTCGAGCGGCTTCAACAT 1523
 QY 841 CTTGCGCAAGAAAGCAATTCGCGATTAATGCGCGCAATTCGCGGCAATTCGCGGCAAT 900
 DB 1524 CTTGCGCAAGAAAGCAATTCGCGATTAATGCGCGCAATTCGCGGCAATTCGCGGCAAT 1583
 QY 901 ATTTCTGCGGCAATTCGCGATTAATGCGCGCAATTCGCGGCAATTCGCGGCAAT 948
 DB 1584 ATTTCTGCGGCAATTCGCGATTAATGCGCGCAATTCGCGGCAATTCGCGGCAAT 1631
 RESULT 22
 AAA81490_11/c
 Continuation (12 of 15) of AAA81490 from base 1100001 (N. meningitidis B full length gen
 WP Sequence split into 15 fragments LOCUS AAA81490 Accession Aaa81490
 WP Fragment Name Begin End
 WP AAA81490_01 1 110000
 WP AAA81490_02 210000 210000
 WP AAA81490_03 310000 310000
 WP AAA81490_04 410000 410000
 WP AAA81490_05 510000 510000
 WP AAA81490_06 610000 610000
 WP AAA81490_07 710000 710000
 WP AAA81490_08 810000 810000
 WP AAA81490_09 910000 910000
 WP AAA81490_10 1010000 1010000
 WP AAA81490_11 1100001 1210000
 WP AAA81490_12 1210000 1310000
 WP AAA81490_13 1310000 1410000
 WP AAA81490_14 1410000 1437668

Query Match 92.6%; Score 877.6; DB 3; Length 110000;
 Best Local Similarity 95.4%; Pred. No. 8,9e-254;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

1 ATGGAATTTTCAATATCTTGTGGCAGCGCGCTTTCGGCTTCAATCTTTGTC 60
 DB ATGGAATTTTCAATATCTTGTGGCAGCGCGCTTTCGGCTTCAATCTTTGTC 95611
 61 GTCAATCCCGCAGCAGGAAGTCCAGCTGTGAAAAGCTCGGGCGTTTCATCGCCCTG 120
 DB GTCAATCCCGCAGCAGGAAGTCCAGCTGTGAAAAGCTCGGGCGTTTCATCGCCCTG 95551
 121 AGGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGGCTGCCATCGCATTCGCTG 180
 DB AGGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGGCTGCCATCGCATTCGCTG 95491
 181 AAGAAGATCCCTTTAGACGTACCCAGCAGCTCTGATCAGCGCGCATTAATGCAATTG 240
 DB AAGAAGATCCCTTTAGACGTACCCAGCAGCTCTGATCAGCGCGCATTAATGCAATTG 95431
 241 ACTGTTGACGGCATCATTAATTCAGTAACCGATCCCAACTGCTCTCATACGGTTG 300
 DB ACTGTTGACGGCATCATTAATTCAGTAACCGATCCCAACTGCTCTCATACGGTTG 95371
 301 AGCACTACATTAATGCAATTAACCGCTTGCCTTCCCAACGACGCTGGTTCCTTATCG 360
 DB AGCACTACATTAATGCAATTAACCGCTTGCCTTCCCAACGACGCTGGTTCCTTATCG 95311
 361 CGATGGAATTTGGAAGAAAGTGTGAAGACGCGCAATCAACGTAACCGTCTGTCG 420
 DB CGATGGAATTTGGAAGAAAGTGTGAAGACGCGCAATCAACGTAACCGTCTGTCG 95251
 421 GCCCTCGATGAAGCCCGCGGCTTGGGAGTGTGAAGTCTCCGTTACGAATCAAGAT 480
 DB GCCCTCGATGAAGCCCGCGGCTTGGGAGTGTGAAGTCTCCGTTACGAATCAAGAT 95191
 481 TTGGTTCGCGCGCAAGAAATCTTGGCGCAATCAGGCAATTAACCGCGCAACCGCA 540
 DB TTGGTTCGCGCGCAAGAAATCTTGGCGCAATCAGGCAATTAACCGCGCAACCGCA 95131
 541 AAACGCGCCGCTTATTCGCGCAATCCGAAGGCGCTGAATCAACCTTGGCAGT 600
 DB AAACGCGCCGCTTATTCGCGCAATCCGAAGGCGCTGAATCAACCTTGGCAGT 95071
 601 GGTACGCTGAAAGCCCAATTCGAATCCGAAGGCGCTGAGCTGCGTCAATGCG 660
 DB GGTACGCTGAAAGCCCAATTCGAATCCGAAGGCGCTGAGCTGCGTCAATGCG 95011
 661 TCCATGCGGAGAAATTCGCGCGCATCAACCGCGCAAGGCGCAAGCGCAATCTTGGCG 720
 DB TCCATGCGGAGAAATTCGCGCGCATCAACCGCGCAAGGCGCGCAATCTTGGCG 94951
 721 CTGTGTCGGAAGCCCAATTCGGAAGGCGCATTCGCAATTGCGCGCTTCAACCCAA 780
 DB CTGTGTCGGAAGCCCAATTCGGAAGGCGCATTCGCAATTGCGCGCTTCAACCCAA 94891
 781 GCGCGGCGGATCGGTCATCTGAAGATTGCGGAACAATACGTAGCGGCTTCAACAT 840
 DB GCGCGGCGGATCGGTCATCTGAAGATTGCGGAACAATACGTAGCGGCTTCAACAT 94831
 841 CTGTGCGAAGAAAGCAATACGCTGATTAATCCCGCAATTTTCCGATCGGCAAGCTG 900
 DB CTGTGCGAAGAAAGCAATACGCTGATTAATCCCGCAATTTTCCGATCGGCAAGCTG 94771
 901 ATTTTCGCGGCAATGAATTTATCGACGAGCAAAACGCGCAATTA 948
 DB ATTTTCGCGGCAATGAATTTATCGACGAGCAAAACGCGCAATTA 94723

RESULT 23
 AAF21609/C
 ID AAF21609 standard; DNA; 349980 BP.
 XX

AC AAF21609;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Neisseria meningitidis B nucleotide sequence S80 ID NO:110.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 XX diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 XX ds.
 OS Neisseria meningitidis.
 XX
 PN MO20006791-A1.
 XX
 PD 09-NOV-2000.
 XX
 XX 08-MAR-2000; 2000WO-US005928.
 PF 30-APR-1999; 99US-0132068P.
 PR 08-OCT-1999; 99WO-US023573.
 PR 28-FEB-2000; 2000GB-00004695.
 XX
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Pizza M, Hickey B, Peterson J, Tettelin H, Venter JC;
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarelli M, Scarlato V;
 PI Rappelli R, Frazer CM, Grandi G;
 XX
 DR WPI; 2000-647603/62.
 XX
 PT Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisserial infections.
 PS
 PS Claim 7; Appendix A; 692pp; English.
 XX
 CC The present invention describes the full length genome of Neisseria
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp
 CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
 CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
 CC AAF21609, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
 CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
 CC primers which are used in the exemplification of the present invention.
 CC The NMB genome and fragments from it have antibacterial activity, and can
 CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
 CC and/or antibodies which binds to the proteins can be used in compositions
 CC for treating or preventing infection due to Neisserial bacteria or as a
 CC diagnostic reagent for detecting the presence of Neisserial bacteria or
 CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
 CC computer storage medium or computer databases can be used in a search to
 CC identify open reading frames (ORFs) or coding sequences within the NMB
 CC genome. The DNA sequences provide further opportunities to find antigenic
 CC or immunogenic proteins which are more effective in vaccines than the
 CC outer membrane proteins currently used
 XX
 SQ Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 U; 0 Other;

Query Match 92.6%; Score 877.6; DB 3; Length 349980;
 Best Local Similarity 95.4%; Pred. No. 1.5e-253;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

1 ATGGAATTTTCAATATCTTGTGGCAGCGCGCTTTCGGCTTCAATCTTTGTC 60
 DB ATGGAATTTTCAATATCTTGTGGCAGCGCGCTTTCGGCTTCAATCTTTGTC 325222
 61 GTCAATCCCGCAGCAGGAAGTCCAGCTGTGAAAAGCTCGGGCGTTTCATCGCCCTG 120
 DB GTCAATCCCGCAGCAGGAAGTCCAGCTGTGAAAAGCTCGGGCGTTTCATCGCCCTG 325162
 121 AGGCGCGGTTTGAATTTTGAATTCCTTTATCGACCGGCTGCCATCGCATTCGCTG 180

```
Db 325161 ACGGCCGGTTGAATATTTGATTCCTTTATGACCGCGTCGCTACCGCATTCGCTG 325102
Qy 181 AAAAGAAATCCCTTTAGAGTACCCAGCCAGGTCTGCATCAGCGGAGTAATACGAATTG 240
Db 325101 AAAAGAAATCCCTTTAGAGTACCCAGCCAGGTCTGCATCAGCGGAGTAATACGAATTG 325042
Qy 241 ACTGTGACGGCATCATCTATTTCCAGTAACCCGATCCCAACTGCGCTCATACGATTG 300
Db 325041 ACTGTGACGGCATCATCTATTTCCAGTAACCCGATCCCAACTGCGCTCATACGATTG 324982
Qy 301 AGCAATCATATTATGCAATTAACCCAGCTTGCCCAACGACGCTGCTGCTTATTCGGG 360
Db 324981 AGCAATCATATTATGCAATTAACCCAGCTTGCCCAACGACGCTGCTGCTTATTCGGG 324922
Qy 361 CGTATGAGTTGAGCAAAACGTTTGAAGAAGCCAGCAAAATCAACAGTACGCTGCTCC 420
Db 324921 CGTATGAGTTGAGCAAAACGTTTGAAGAAGCCAGCAAAATCAACAGTACGCTGCTCG 324862
Qy 421 GCCCTCGATGAAAGCCGCGGGCTTGGGGTGTAAGTCTCCGTTACGAATCAAGGAT 480
Db 324861 GCTTTGACGAGGCGCGGGCTTGGGGTGTAAGTCTCCGTTACGAATCAAGGAT 324802
Qy 481 TTGTTCCGCGCAAGAAATCCTTCGCGCAATGCAAGCAAAATTACCGCGCAACGCGAA 540
Db 324801 TTGTTCCGCGCAAGAAATCCTTCGCGCAATGCAAGCAAAATTACCGCGCAACGCGAA 324742
Qy 541 AAACGCGCGCTTATTCGCGCAATCCGAAGCCGTAAATTCGAACAAATACCTTGCCAGT 600
Db 324741 AAACGCGCGCTTATTCGCGCAATCCGAAGCCGTAAATTCGAACAAATACCTTGCCAGT 324682
Qy 601 GGTGACGCTGAAAGCCGAATCCGAATCCGAAGCCGAGGCTCAGGCTGCGTCAATGCG 660
Db 324681 GGTGACGCTGAAAGCCGAATCCGAATCCGAAGCCGAGGCTCAGGCTGCGTCAATGCG 324622
Qy 661 TCCAAATGCGAAGAAATGCGCGCATCAACCGCGCAAGGCGAAAGCGAAATCCCTGCGC 720
Db 324621 TCAATGCGAAGAAATGCGCGCATCAACCGCGCAAGGCGAAAGCGAAATCCCTGCGC 324562
Qy 721 CTGTGTGCGCAAGCAATGCGCGCAATCCGTGCAAAATTTGCGCGCGCTTCAAAACCAA 780
Db 324561 CTGTGTGCGCAAGCAATGCGCGCAATCCGTGCAAAATTTGCGCGCGCTTCAAAACCAA 324502
Qy 781 GCGCGGCGGAGTGGCGTCAATCTGAAAGTGGGGAACATAGTAGCGCGCTTCAACAT 840
Db 324501 GCGCGGCGGAGTGGCGTCAATCTGAAAGTGGGGAACATAGTAGCGCGCTTCAACAT 324442
Qy 841 CTTGCGCAAGAAAGCAATAGCTGATTAATGCGCGCAATGTTGCCGACATCGGACGCTG 900
Db 324441 CTTGCGCAAGAAAGCAATAGCTGATTAATGCGCGCAATGTTGCCGACATCGGACGCTG 324382
Qy 901 ATTCTGTGCGCGCAATTAATTAATGACGAGCAAGCAAAACCGCAAAATTA 948
Db 324381 ATTCTGTGCGCGCAATTAATTAATGACGAGCAAGCAAAACCGCAAAATTA 324334

RESULT 24
AAF21610/c
ID AAF21610 standard; DNA; 349980 BP.
XX
AC AAF21610;
XX
DT 13-MAR-2001 (first entry)
XX
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
XX
KM Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
XX diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX de.
XX Neisseria meningitidis.
XX
FN WO20006791-A1.
```

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XX
PD 09-NOV-2000.
XX
PF 08-MAR-2000; 2000WO-US005928.
XX
PR 30-APR-1999; 99US-0132068P.
XX
PR 08-OCT-1999; 99WO-US023573.
XX
PR 28-FEB-2000; 2000GB-00004695.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Frazer CM, Grandi G;
XX
DR WPI; 2000-647603/62.
XX
PT Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect, treat and prevent Neisserial infections.
XX
PS Claim 7; Appendix A; 692pp; English.
XX
CC The present invention describes the full length genome of Neisseria
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences which
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the Neisseria proteins
CC given in AAB58550 to AAB58593, and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. Neisseria nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions
CC for treating or preventing infection due to Neisserial bacteria or as a
CC diagnostic reagent for detecting the presence of Neisserial bacteria or
CC of antibodies raised to Neisserial bacteria. Computers, computer memory,
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines than the
CC outer membrane proteins currently used
XX
SQ Sequence 349980 BP; 86771 A; 92803 C; 86340 G; 84066 T; 0 U; 0 Other;
Query Match 92.6%; Score 877.6; DB 3; Length 349980;
Best local similarity 95.4%; Pred. No. 1.5e-253;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 1 ATGGAATTTTTCATATCTGTTGGCAGCGCGTGGCGCTTTCGGCTCAATCCTTTGTC 60
Db 25281 ATGGAATTTTTCATATCTGTTGGTGGAGCGTCCCGCTTTCGGTTCAAAATCCTTTGTT 25222
Qy 61 GTCATCCCGCAGAGAGTCCAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCCTG 120
Db 25221 GTCATCCCGCAGAGAGTCCAGTGTGCAAAAGCTCGGCGCTTTCATCGCGCCCTG 25162
Qy 121 ACGGCGCGTTGAATTAATTTGATTCCTTTATGACGCGCGTGGCTTACCGCATTCGCTG 180
Db 25161 ACGGCGCGTTGAATTAATTTGATTCCTTTATGACGCGCGTGGCTTACCGCATTCGCTG 25102
Qy 181 AAAAGAAATCCCTTTAGAGTACCCAGCCAGGTCTGCATCAGCGGAGTAATACGAATTG 240
Db 25101 AAAAGAAATCCCTTTAGAGTACCCAGCCAGGTCTGCATCAGCGGAGTAATACGAATTG 25042
Qy 241 ACTGTGACGGCATCATCTATTTCCAGTAACCCGATCCCAACTGCGCTCATACGATTG 300
Db 25041 ACTGTGACGGCATCATCTATTTCCAGTAACCCGATCCCAACTGCGCTCATACGATTG 24982
Qy 301 AGCAATCATATTATGCAATTAACCCAGCTTGCCCAACGACGCTGCTGCTTATTCGGG 360
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Db 24981 AGCACTACATTATGCGCATTTACCAAGCTTGCCCAAGACGCGTGTTCGTTATCGGG 24922
Qy 361 CGTATGAGTTGGACAAAAGCTTTGAAGAACCGGACGAATCAACGTAACGTCCTCC 420
Db 24921 CGTATGAGTTGGACAAAAGCTTTGAAGAACCGGACGAATCAACGTAACGTCCTCC 24862
Qy 421 GCCCTGATGAAAGCGCGGGGCTTGGGGTGAAGATCTCCGTTACCAATCAAGAT 480
Db 24861 GCTTTGACAGAGCGCGCGGGCTTGGGGTGAAGATCTCCGTTATGAGTTAAAGAC 24802
Qy 481 TTGTTCCGCGCGCAAGAAATCCTTCGCGCAATGACGCACAAAATTAACGCGCAAGCGAA 540
Db 24801 TTGTTCCGCGCGCAAGAAATCCTTCGCGCAATGACGCGCAAAATTAACGCGCAAGCGAA 24742
Qy 541 AAACGCGCGCGTATTTGCGCAATCCGAAAGCGCGCTTAATGAACAATCAACTTGCAGT 600
Db 24741 AAACGCGCGCGTATTTGCGCAATCCGAAAGCGCGCTTAATGAACAATCAACTTGCAGT 24682
Qy 601 GGTTCAGCGGAAAGCGGAAATCCAGCAATCCGAAAGCGCGCTCAGGCTGCGTCAATGCG 660
Db 24681 GGTTCAGCGGAAAGCGGAAATCCAGCAATCCGAAAGCGCGCTCAGGCTGCGTCAATGCG 24622
Qy 661 TCCAAATGCGGAAATCGCGCGCATCAACGCGCAAGCGGAAAGCGGAAATCCCTGCGC 720
Db 24621 TCCAAATGCGGAAATCGCGCGCATCAACGCGCGCAAGCGGAAAGCGGAAATCCCTGCGC 24562
Qy 721 CTTGTTGCGGAAAGCGGAAATCGCGCGCATCAACGCGCGCTTAATGAACAATCAACTTGCAGT 780
Db 24561 CTTGTTGCGGAAAGCGGAAATCGCGCGCATCAACGCGCGCTTAATGAACAATCAACTTGCAGT 24502
Qy 781 GCGCGGCGGAGATCGCGTCAATCTGAAGATTTGGGAAACATATGACCGCGTTCACCAAT 840
Db 24501 GCGCGGCGGAGATCGCGTCAATCTGAAGATTTGGGAAACATATGACCGCGTTCACCAAT 24442
Qy 841 CTTGCGCAAGAAAGCAATACGCTGATTTATGCGCGCAATGTTGCGGACGCGCTG 900
Db 24441 CTTGCGCAAGAAAGCAATACGCTGATTTATGCGCGCAATGTTGCGGACGCGCTG 24382
Qy 901 ATTTCGCGGAGATGAAATTTATGACAGACGCAAAACCGCAATTA 948
Db 24381 ATTTCGCGGAGATGAAATTTATGACAGACGCAAAACCGCAATTA 24334

RESULT 25
AAZ53749
ID AAZ53749 standard; DNA; 850 BP.
XX
AC AAZ53749;
XX
DT 15-SEP-2003 (revised)
DT 21-MAR-2000 (first entry)
XX
DE Neisseria gonorrhoeae ORF 519 partial DNA sequence SEQ ID NO:1447.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; de.
XX
OS Neisseria gonorrhoeae.
XX
PN WO9557280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US009346.
XX
PR 01-MAY-1998; 98US-0083758P.
PR 31-JUL-1998; 98US-0094869P.
PR 02-SEP-1998; 98US-0098994P.
PR 02-SEP-1998; 98US-0099062P.
PR 09-OCT-1998; 98US-0103749P.
PR 09-OCT-1998; 98US-0103794P.
PR 09-OCT-1998; 98US-0103796P.
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PR 25-FEB-1999; 99US-0121528P.
XX
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;
PI Petersen J, Pizza M, Rappuoli R, Ratcl G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI, 2000-062150/05.
DR P-PSDB; AA74987.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.
XX
PS Claim 7, Page 776; 1453pp; English.
XX
CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia) to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols. (Updated on 15-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 850 BP; 215 A; 250 C; 205 G; 180 T; 0 U; 0 Other;

Query Match 88.6%; Score 840.4; DB 3; Length 850;
Best Local Similarity 99.3%; Pred. No. 1.7e-243;
Matches 844; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGAATTTTCATTATCTTGTGGACGCGTCCGCTTTTGGGTTCAATCCTTTGTC 60
Db 1 ATGGAATTTTCATTATCTTGTGGACGCGTCCGCTTTTGGGTTCAATCCTTTGTC 60
Qy 61 GTTCATCCCGGACGAGAGTCCAGTGTGGAAGGCTCGGGCGTTTCATCGCGCCCTG 120
Db 61 GTTCATCCCGGACGAGAGTCCAGTGTGGAAGGCTCGGGCGTTTCATCGCGCCCTG 120
Qy 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
Db 121 ACGGCGGTTTGAATATTTTGAATTCCTTTATCGACCGCGTCCCTACCGCATTCGCTG 180
Qy 181 AAAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAGCGCGATTAATCGCAATTG 240
Db 181 AAAAATCCCTTTAGACGTACCCAGCGAGTTCGATCAGCGCGATTAATCGCAATTG 240
Qy 241 ACTGTTGACGCGATATCTATTTTCCAAATCCGATCCCAATCGCTCATAGGTTGCG 300
Db 241 ACTGTTGACGCGATATCTATTTTCCAAATCCGATCCCAATCGCTCATAGGTTGCG 300
Qy 301 AGCACTACATTATGAGCAATTAACCAAGCTTGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAATTAACCAAGCTTGCCCTGCTCC 420
Db 301 AGCACTACATTATGAGCAATTAACCAAGCTTGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAATTAACCAAGCTTGCCCTGCTCC 420
Qy 421 GCGCTGATGAAAGCGCGGGGCTTGGGGTGAAGATCTCCGTTAGAAATCAAGAT 480
Db 421 GCGCTGATGAAAGCGCGGGGCTTGGGGTGAAGATCTCCGTTAGAAATCAAGAT 480
Qy 481 TTGTTCCGCGCGCAAGAAATCCTTCGCGCAATGACGCGCAAAATTAACGCGCAAGCGGAA 540
Db 481 TTGTTCCGCGCGCAAGAAATCCTTCGCGCAATGACGCGCAAAATTAACGCGCAAGCGGAA 540
```

QY 541 AAAGCGCCGCTATTGCGGAATCCGAAGCGCGTAATAATCGAAACAATCAACTTGGCCAGT 600
DB 541 AAAGCGCCGCTATTGCGGAATCCGAAGCGCGTAATAATCGAAACAATCAACTTGGCCAGT 600
QY 601 GGTGAGCGGTGAAGCGGAATCCGAATCCGAAGCGCGTAAGTGGCTGCGTCAATGCG 660
DB 601 GGTGAGCGGTGAAGCGGAATCCGAATCCGAAGCGCGTCAAGTGGCTGCGTCAATGCG 660
QY 661 TCCGAATGCCGAATAATCGCCGATCAACCGCGCAAGCGGAAGCGGAATCCCTGGCC 720
DB 661 TCCGAATGCCGAATAATCGCCGATCAACCGCGCAAGCGGAATCCCTGGCC 720
QY 721 CTTGTGCGCGAAGCAATGCGCAAGCCATCCGTCAATTTGCGCGCCCTTCAACCCAA 780
DB 721 CTTGTGCGCGAAGCAATGCGCAAGCCATCCGTCAATTTGCGCGCCCTTCAACCCAA 780
QY 781 GCGCGGCGGATGCGGTCAATCTGAAGATTGCGGAACAATCGTAGCGCGTCAACAT 840
DB 781 AGCGGCGGATGCGGTCAATCTGAAGATTGCGGACATATGTTACCGCGTCAAAAT 840
QY 841 CTTGCCAAG 850
DB 841 CTTGCCAAG 850

RESULT 26

AAZ54580
ID AAZ54580 standard; DNA, 600 BP.

AC AAZ54580;

DT 21-MAR-2000 (first entry)

DB Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:3045.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KM antibacterial; gene therapy; ds.

XX Neisseria meningitidis.

PN MO9957280-A2.

PD 11-NOV-1999.

PF 30-APR-1999; 99WO-US009346.

PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 25-FEB-1999; 99US-0121528P.

PA (CHIR) CHIRON CORP.
PI (GENO-) INST GENOMIC RES.

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Peteren J, Pizzo M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettein H, Venter JC;

DR WPI; 2000-062150/05.
DR P-PSDB; AAY75778.

PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics.

PS Example 1; Page 73-74; 1453pp; English.

XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941

CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of the
CC invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the manufacture
CC of medicaments for treating or preventing infection due to Neisserial
CC bacteria (e.g. meningitis and septicemia), to detect the presence of
CC Neisseria bacteria, or to raise antibodies. They may also be used to
CC screen for agonists or antagonists, which may themselves have use as
CC antibacterial agents. The polynucleotides of the invention may also be
CC used in gene therapy protocols

XX Sequence 600 BP; 166 A; 158 C; 159 G; 117 T; 0 U; 0 Other;

QY Query Match 57.7%; Score 547.2; DB 3; Length 600;

QY Best Local Similarity 94.5%; Pred. No. 7.9e-155;

QY Matches 567; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 349 TCCGTTATCCGCGCTATGAGTTGACAAACGTTTGAAAGACGACGAATCAACAGT 408
DB 1 TCCGTTATCCGCGCTATGAGTTGACAAACGTTTGAAAGACGACGAATCAACAGT 60

QY 409 ACCGTGCTTCGCGCTTCGATGAAGCGCGCGGCTTGGGGTGAAGTCTCCGTTAC 468
DB 61 ACTGTGTGCGGCTTTGACGAGCGCGCGGCTTGGGGTGAAGTCTCCGTTAT 120

QY 469 GAAATCAAGATTGTTCCGCGCAAGAAATCTTCGCGCAATGACGACGAATTAAC 528
DB 121 GAGATTAAAGCTTGTTCCGCGCAAGAAATCTTCGCGCAATGACGACGAATTAAC 180

QY 529 GCCGAAACGCAAAACCGCGCGCTATTGCCAATCCGAAGCGCGTAATCAACATC 588
DB 181 GCGAAGCGCAAAACCGCGCGCTATTGCCAATCCGAAGCGCGTAATCAACATC 240

QY 589 AACCTTGCAGTGTGAGCTGAAGCGCAATCCGAATCCGAAGCGCGTCAAGCT 648
DB 241 AACCTTGCAGTGTGAGCTGAAGCGCAATCCGAATCCGAAGCGCGTCAAGCT 300

QY 649 GCGGTCAATGATGCAATGCGAAGAAATGCGCGCATCAACGCGCAAGCGGAAGCG 708
DB 301 GCGGTCAATGATGCAATGCGAAGAAATGCGCGCATCAACGCGCAAGCGGAAGCG 360

QY 709 GAATCCCTGCGCTTGTGTGCGAAGCGCAATGCGCAATCCGTCGAATTTCCGCGCC 768
DB 361 GAATCCCTGCGCTTGTGTGCGAAGCGCAATGCGCAATCCGTCGAATTTCCGCGCC 420

QY 769 CTTCAAAACCAAGCGCGGCGGATGCGGTCAATCTGAAGTTGCGGAACAATAGTGCC 828
DB 421 CTTCAAAACCAAGCGCGGCGGATGCGGTCAATCTGAAGTTGCGGAACAATAGTGCC 480

QY 829 GCGTTCAACATCTTGCCAAGAAAGCAATGCGTATTTGCGCGCAATGTTGCGGAC 888
DB 481 GCGTTCAACATCTTGCCAAGAAAGCAATGCGTATTTGCGCGCAATGTTGCGGAC 540

QY 889 ATCGGACGCTGATTTGCGCGGATGAATTTCAACGACGACCAAAACCGCCAAATA 948
DB 541 ATCGGACGCTGATTTGCGCGGATGAATTTCAACGACGACCAAAACCGCCAAATA 600

RESULT 27

AAAB1263
ID AAAB1263 standard; DNA, 600 BP.

AC AAAB1263;

DT 04-DEC-2000 (first entry)

DB N. meningitidis partial DNA sequence m519. seq SEQ ID NO:968.

XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KM Meningococcus B; MemB; ds.

XX Neisseria meningitidis.
 OS
 XX
 XX WO200022430-A2.
 PN
 XX
 XX 20-APR-2000.
 PD
 XX
 XX 08-OCT-1999; 99WO-US023573.
 PF
 XX
 XX 09-OCT-1998; 98US-0103794P.
 PR
 XX 30-APR-1999; 99US-0132068P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC, Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rapunoli R, Pizzo M;
 PI
 XX WPI, 2000-318079/27.
 DR
 XX P-PSDB; AAB55623.
 XX
 XX
 XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
 PT in the diagnosis and treatment of N. meningitidis infection and other
 PT Neisserial infections, for example, N.gonorrhoea.
 XX
 XX Claim 9, Page 70; 1760pp; English.
 XX
 XX The present invention describes methods of obtaining immunogenic proteins
 CC from Neisseria genomic sequences. AAB1453 to AAB2414 represent
 CC specifically claimed Neisseria meningitidis genomic DNA sequences;
 CC AAB1260 to AAB1303 and AAB25620 to AAB25663 represent Neisseria DNA
 CC sequences and their corresponding proteins; AAB1254 to AAB1259 and
 CC AAB1304 to AAB1321 represent PCR primers used in the isolation of
 CC Neisseria meningitidis DNA sequences; and AAB1322 to AAB1452 represent
 CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
 CC used in the exemplification of the present invention. The nucleic acid
 CC sequences, protein sequences, and antibodies against them, can be used in
 CC the manufacture of a composition. The composition can be used as a
 CC medicament (or in the manufacture of a medicament) for treating,
 CC preventing or diagnosing infection due to Neisserial bacteria. For
 CC example, some of the identified proteins could be components of vaccines
 CC against Meningococcus B; against all serotypes; and/or against all
 CC pathogenic Neisseriae. Identification of sequences from the bacterium
 CC will also facilitate production of biological probes, particularly
 CC organism-specific probes. Attempts to make efficacious Meningococcus B
 CC vaccines have failed mainly due to antigen tolerance. Multivalent
 CC vaccines have also been tried but none have successfully overcome
 CC antigenic variability. The provision of further, complete sequences may
 CC provide an opportunity to identify secreted or surface exposed proteins
 CC that may be presumed targets for the immune system and which are not
 CC antigenically variable or at least more conserved than other more
 CC variable regions
 XX
 XX Sequence 600 BP; 166 A; 158 C; 159 G; 117 T; 0 U; 0 Other;
 SQ
 Query Match 57.7%; Score 547.2; DB 3; Length 600;
 Best Local Similarity 94.5%; Pred.No.7.9e-155;
 Matches 567; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 349 TCCGTTATCGGGCGTTCGATGAGCAAAACGTTGAAAGACGACGCAAAATCAACAGT 408
 DB 1 TCCGTTATCGGGCGTTCGATGAGCAAAACGTTGAAAGACGACGCAAAATCAACAGT 60
 QY 409 ACCGTCGTCGCGCCTCGATGAAAGCGCGGGGCTTGGGGTGTGAAAGTCTCGCTAC 468
 DB 61 ACTGTTGTCGCGCTTTCGACAGAGCGCGCGGCTTGGGGTGTGAAAGTCTTCAT 120
 QY 469 GAAATCAAGATTGTTGCTTCGCGCAAGAAATCTTTCGCGCAATGACGACCAAAATAC 528
 DB 121 GAGATTAAAGACTTGGTTCCGCGCAAGAAATCTTTCGCTCAATGACGCGCAAAATAC 180
 QY 529 GCCGAACGGAAAAAGCGCGCTATTCGCAATCCGAAGCGCTTAAATCGAAACAATC 588

DB 181 GCCGAACGGAAAAAGCGCGCTATTCGCGCAATCCGAAGTCTTAAATCGAAACAATC 240
 QY 589 AACCTTGCATGTGTCACGCTGGAAGCCGGAATTCGAATCCGAAGGAGGCTCAGGCT 648
 DB 241 AACCTTGCATGTGTCACGCTGGAAGCCGGAATTCGAATCCGAAGGAGGCTCAGGCT 300
 QY 649 GCGGTCAATGCGTTCATATGCGAGAAATTCGCCCATCAACCGCGCCAAAGCGCAAGCG 708
 DB 301 GCGGTCAATGCGTTCATATGCGAGAAATTCGCCCATCAACCGCGCCAAAGGTGAAGG 360
 QY 709 GAATCCCTGCGCTTGTTCGCGAAGCCGAATCCGAAGCCATTCGTAATTCGCCCGCC 768
 DB 361 GAATCCCTGCGCTTGTTCGCGAAGCCGAATCCGAAGCCATTCGTAATTCGCCCGCC 420
 QY 769 CTTCAACCCCAAGCGCGCGCGATGCGGTCAATCTGAAGATTGCGGAACAATACCTAGCC 828
 DB 421 CTTCAACCCCAAGCGCGCGATGCGGTCAATCTGAAGATTGCGGAACAATACCTAGCC 480
 QY 829 GCGTCAACCAATCTTGCAGAAAGAAAGAAATACGCTGATTATGCGCGCAATGTCGAC 888
 DB 481 GCGTCAACCAATCTTGCAGAAAGAAAGAAATACGCTGATTATGCGCGCAATGTCGAC 540
 QY 889 ATCGGCAAGCTGATTTTCGCGCGCATGAATAATTATGACAGCAGCAAAACCGCAATPA 948
 DB 541 ATCGGCAAGCTGATTTTCGCGCGCATGAATAATTATGACAGCAGCAAAACCGCAATPA 600
 RESULT 28
 AAF21548
 ID AAF21548 strand; DNA; 600 BP.
 XX
 XX AAF21548;
 AC
 XX
 XX 13-MAR-2001 (first entry)
 DT
 XX
 XX N. meningitidis partial DNA sequence ms19.seq SEQ ID NO:8.
 DE
 XX
 XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KM diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KW ds.
 XX
 XX Neisseria meningitidis.
 OS
 XX
 XX WO200066791-A1.
 PN
 XX
 XX 09-NOV-2000.
 PD
 XX
 XX 08-MAR-2000; 2000WO-US005928.
 PF
 XX
 XX 30-APR-1999; 99US-0132068P.
 PR
 XX 08-OCT-1999; 99WO-US023573.
 PR 28-FEB-2000; 2000GB-00004695.
 XX
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rapunoli R, Frazer CM, Grandi G;
 PI
 XX WPI, 2000-647603/62.
 DR
 XX P-PSDB; AAB58553.
 XX
 XX Neisseria meningitidis B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent Neisserial infections.
 PT
 XX
 XX Example 1; Page 71; 692pp; English.
 PS
 XX The present invention describes the full length genome of Neisseria
 CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
 CC represent fragments of the NMB genomic sequence, as the sequence was too
 CC long to go in a record on its own it was split into 8 sequences which
 CC overlap each other at the beginning and end of each sequence by 49980 bp

(i.e. the last 49980 bp of AAP21544 is repeated at the beginning of AAP21607, the last 49980 bp of AAP21607 are repeated at the beginning of AAP21608, and so on). AAP21545 to AAP21588 encode the *Neisseria* proteins given in AAB5550 to AAB58593, and AAP21589 to AAP21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. *Neisseria* nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to *Neisseria* bacteria or as a diagnostic reagent for detecting the presence of *Neisseria* bacteria or of antibodies raised to *Neisseria* bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used

Sequence 600 BP; 166 A; 158 C; 159 G; 117 T; 0 U; 0 Other;

Query Match 57.4%; Score 547.2; DB 3; Length 600;

Best Local Similarity 94.5%; Pred. No. 7.9e-155;

Matches 567; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

```
Oy      349  TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGCGACGAATCAACAGT
Db      1    TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGCGACGAATCAACAGT
Oy     409  ACCGTCGTCCTCGCCCTCGATGAAAGCCCGCGGCTTGGGGTGTGAAGTCTCCGTTAC
Db     61    ACTGTTGTGGCGCTTGTGACGAGCGCGCGGCGCTTGGGGTGTGAAGTCTCCGTTAT
Oy     469  GAAATCAAGATTGTTTCCGCGCGCAAGAAATCTTCGCGCAATCGAGCAACAATTACC
Db    121  GAGATTAAAGACTTGTTCCGCGCGCAAGAAATCTTCGCTCAATCGAGCGCAATTACT
Oy     529  GCCGAAACGCAAAAACGCGCGCTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC
Db    181  GCCGAAACGCAAAAACGCGCGCTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC
Oy     589  AACCTTGCAATGTGTGACGCTGAAAGCCGAATTCACAAATTCGAAGGAGAGCTCAAGCT
Db    241  AACCTTGCAATGTGTGACGCGGAAACCGAAATTCACAAATTCGAAGGAGAGCTCAAGCT
Oy     649  GCGGTCATGCGTCCCAATGCGAGAAATTCGCCGCAATCAACGCGCGCAAAAGGCAAGCG
Db    301  GCGGTCATGCGTCCCAATGCGAGAAATTCGCCGCAATCAACGCGCGCAAAAGGTAAGCG
Oy     709  GAATCCCTGCGCTTGTGCGGAAAGCCAAATGCGCAAGCCATCCGTCAAATTCGCGCGCC
Db    361  GAATCCCTGCGCTTGTGCGGAAAGCCAAATGCGCAAGCCATCCGTCAAATTCGCGCGCC
Oy     769  CTTCAAAACCCAAAGGCGGCGCGATGCGTCAATCTGAAGATTGCGGAAACAATAGTAGCC
Db    421  CTTCAAAACCCAAAGGCGGCGCGATGCGTCAATCTGAAGATTGCGGAAACAATAGTAGCC
Oy     829  GCGTTCAACAATCTTGGCAAGAAAGCAATCGCGATTAATGCGCGCAATGTTGCGGAC
Db    481  GCGTTCAACAATCTTGGCAAGAAAGCAATCGCGATTAATGCGCGCAATGTTGCGGAC
Oy     889  ATCGGCAACCTGATTCTGCGCGCGCATGAATAATTACGACAGCAAAACCGCCAAATTA
Db    541  ATCGGCAACCTGATTCTGCGCGCGCATGAATAATTACGACAGCAAAACCGCCAAATTA
```

RESULT 29

AAZ53750 standard; DNA; 600 BP.

AAZ53750;

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 519 partial DNA sequence SEQ ID NO:1449.

Neisseria meningitidis; *Neisseria gonorrhoeae*; antigen; vaccine; antigenic; diagnostic; immunogenic; infection; meningitis; septicemia; antibacterial; gene therapy; ds.

Neisseria meningitidis.

MO9957280-A2.

11-NOV-1999.

30-APR-1999; 99WO-US009346.

01-MAY-1998; 98US-0083758P.

31-JUL-1998; 98US-0094869P.

02-SEP-1998; 98US-0098994P.

02-SEP-1998; 98US-0099062P.

09-OCT-1998; 98US-0103749P.

09-OCT-1998; 98US-0103794P.

25-FEB-1999; 99US-0121528P.

(CHIR) CHIRON CORP.

(GENO-) INST GENOMIC RES.

Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M, Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M, Tettelin H, Venter JC;

WPI; 2000-062150/05.

P-PSDB; AAY74988.

Novel *Neisseria* polypeptides predicted to be useful antigens for vaccines and diagnostics.

Claim 7; Page 777; 1453P; English.

AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941

represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54473 represent

PCR primers used in the exemplification of the present invention. The

polypeptides, the polynucleotides, antibodies and compositions of the

invention can be used as vaccines, as diagnostic reagents, and as

immunogenic compositions. The polypeptides can be used in the manufacture

of medicaments for treating or preventing infection due to *Neisseria*

bacteria (e.g. meningitis and septicemia), to detect the presence of

Neisseria bacteria, or to raise antibodies. They may also be used to

screen for agonists or antagonists, which may themselves have use as

antibacterial agents. The polynucleotides of the invention may also be

used in gene therapy protocols

Sequence 600 BP; 165 A; 158 C; 159 G; 118 T; 0 U; 0 Other;

Query Match 57.4%; Score 544; DB 3; Length 600;

Best Local Similarity 94.2%; Pred. No. 7.4e-154;

Matches 565; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```
Oy      349  TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGCGACGAATCAACAGT
Db      1    TCCGTTATCGGCGGTATGAGTGGACAAACGTTTGAAGAACGCGACGAATCAACAGT
Oy     409  ACCGTCGTCCTCGCCCTCGATGAAAGCCGCGGCTTGGGGTGTGAAGTCTCCGTTAC
Db     61    ACTGTTGTGGCGCTTGTGACGAGCGCGCGGCTTGGGGTGTGAAGTCTCCGTTAT
Oy     469  GAAATCAAGATTGTTTCCGCGCGCAAGAAATCTTCGCGCAATCGAGCAACAATTACC
Db    121  GAGATTAAAGACTTGTTCCGCGCGCAAGAAATCTTCGCTCAATCGAGCGCAATTACT
Oy     529  GCCGAAACGCAAAAACGCGCGCTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC
Db    181  GCCGAAACGCAAAAACGCGCGCTTATGCGCAATCGAAGCGCGTAAATCGAACAAATC
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Oy 589 AACCTTGCCAGTGTGTCAGCGTCAAGCCGAAATTCACATCCGAAGCGGCTGAGCT 648
Db 241 AACCTTGCCAGTGTGTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 300
Oy 649 GGGGTCATGCGTCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 708
Db 301 GGGGTCATGCGTCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Oy 709 GAATCCCTGCGCGCTGTTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 768
Db 361 GAATCCCTGCGCGCTGTTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Oy 769 CTTCAAAACCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 828
Db 421 CTTCAAAACCGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Oy 829 GCGTCAACCAATCTTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 888
Db 481 GCGTCAACCAATCTTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Oy 889 ATCGGCGAGCTGATTTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 948
Db 541 ATCGGCGAGCTGATTTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600

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RESULT 30

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AAAI2730
ID AAAI2730 standard; DNA; 1677 BP.

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AAAI2730;

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25-JUL-2000 (first entry)

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DNA encoding of a plant stomatin-like polypeptide.

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Maize; stomatin-like polypeptide; transgenic plant; disease resistance;
plant pathogen defense system; plant pest; fungal pathogen; virus;
nematode; insect; stomatin; univalent cation permeability; ion transport;
transformation efficiency; cell cycle; cell proliferation; cell growth;
85.

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Zea mays.

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Key Location/Qualifiers
FH 161..1345
FT /tag= a
FT /product= "stomatin-like polypeptide"

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WO200015817-A2.

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23-MAR-2000.

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15-SEP-1999; 99WO-US021384.

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17-SEP-1998; 98US-0100748P.

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(PION-) PIONEER HI-BRED INT INC.

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Gordon-Kamm WJ, Lowe KS, Nadimpalli R, Simmons CR;

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MPI; 2000-271453/23.

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P-PSDB; AAY84663.

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New isolated plant stomatin-like gene used for producing transgenic
plants with enhanced disease resistance and for manipulating ion
transport in transformed plants and plant cells.

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Claim 20; Page 66-67; 68pp; English.

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The present sequence encodes a maize stomatin-like polypeptide. The
polynucleotide is used to produce transgenic plants with enhanced disease
resistance through activation of the plant pathogen defense system. Plant
pests which can be controlled in this manner include fungal pathogens,

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CC viruses, nematodes and insects. Stomatin is an integral membrane protein
CC which functions as a negative regulator of univalent cation permeability.
CC The stomatin-like polynucleotide can therefore be used to manipulate ion
CC transport in transformed plants and plant cells which can result in
CC blocked or reduced cell cycle arrest, and increased transformation
CC efficiency. It can also be used for enhancing plant culture methods,
CC modulating the cell cycle and cell proliferation, and positively and
CC negatively manipulating cell growth

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SQ Sequence 1677 BP; 460 A; 441 C; 406 G; 370 T; 0 U; 0 Other;

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Query Match 18.4%; Score 174; DB 3; Length 1677;

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Best Local Similarity 52.4%; Pred. No. 1.1e-41;
Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;

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Oy 60 GCGTATCCCGCCAGCAGGAAGTCCAGTGTGGAAGGCTCGGCGCTTCATCGGCGCT 119
Db 337 CATAGTCCGCGAGGAGGAGGCTTACGTTGTGAGAGATTGCGGAGTATTCAGACCT 396
Oy 120 GACGCGCGGTTGAAATTTTGAATCCCTTATGACCGCGTCCGCTACCGCATTCGCT 179
Db 397 CGGCTCCGCGTTCACCTTCGATCCCGCGTCAACGATTTGCTTACGTCATCGCT 456
Oy 180 GAAAGAAATCCCTTAGAGTACGACCGCAGGCTGATCAGCGCGATATATACCAAT 239
Db 457 CAGGAGAGACATCCCTATCCCTCACCAGAACGCGATCAGAGCAAGTACCAT 516
Oy 240 GACTGTGACGCGATCATCTATTTCCAGATTAACGATCCCAATCGCTCATAGGTTTC 299
Db 517 ACAGATGACGCGTATCTATGATCAAGATCAGACCTCATCTGCTTCTATGCTGT 576
Oy 300 GAGCAATCAATATGAGCAATTAACCGATTCGCGGCGGCGGCGGCGGCGGCGGCGG 359
Db 577 GGAGATCCCAATCTATGCTGCTCTACCACTTGCAAAACATGAGAGTGAAGTCTCG 636
Oy 360 GCGTATGAGTGAAGCAAAACGTTGGAAGAGCGGCGGCGGCGGCGGCGGCGGCGG 419
Db 637 GAGATATCACTTATGATGAGATCTTTGAGAGAGATGATGATGAGAGAGATTTGAG 696
Oy 420 CGCGCTGATGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479
Db 697 TGCATCATGAGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 756
Oy 480 TTTGTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539
Db 757 CATTAATCTCTCAGAGGAGGATGAGCGCTATGAGATGAGCGGCGGCGGCGGCGG 816
Oy 540 AAAAGCGCGCGGATTTGCGGATCCGAAAGCGGTAATTCGAACCAATCAACTTCCAG 599
Db 817 AAAAGCGCGCTCAAAATCTTGAATCAGAGGAGTGAAC----- 854
Oy 600 TGGTCAGCTGAGAGCGGAAATCCAAATCCGAGGCGAGGCTCAGGCTGCGCTCATTC 659
Db 855 -----AGGCGCAATCTTGAATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 903
Oy 660 GTCCAAATGCGGAGAAATGCGCGCATCAACCGCGCGGCGGCGGCGGCGGCGGCGG 719
Db 904 ATCTGAGAGGCTATGTTGATGATGACCAACCGTGCAGAGGCTGCGGCGGCGGCGG 963
Oy 720 CCTTGTGCGGAGCGCAATGCGGAGGCGCATCCGTCAAAATTTGCGCGCGCGCTTCAACCA 779
Db 964 TGCAGAGTGAAGGCTACTGCTGCGGAGGAGGATTTGTTTCAATGATGATGACCACTGA 1023
Oy 780 AGCGCGGCGGAGTGCAGTCAATCTGAGATGCGGAGGAGGAGGAGGAGGAGGAGGAG 839
Db 1024 AGCGAGTGCAGAGGCTGAGTGAAGTGAATCTGAGAGGAGGAGGAGGAGGAGGAGGAG 1083
Oy 840 TCTTGCAAGAGAGCAATAGCTGATTTATGCGCGCGCAATGTTGCC 885
Db 1084 TCTGCGCAAAAGAGCAATATACATGCTTCTTCAAGGTATGATGCC 1129

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RESULT 31

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AAH6657
ID AAH6657 standard; DNA; 1296 BP.
XX
AC AAH6657;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 1692.
XX
KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
KM organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159152.
PR 03-AUG-2000; 2000JP-00280988.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
DR WP1; 2001-376931/40.
DR P-PSDB; AAG91438.
XX
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Claim 8; SEQ ID NO 1692; 246bp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of Corynebacterium bacterium, measuring expression amount and analyzing
CC the expression profile or expression pattern of a gene derived from
CC Corynebacterium bacterium, and identifying a homologue of a gene derived from
CC Corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the European Patent Office
XX
SQ Sequence 1296 BP; 351 A; 392 C; 327 G; 226 T; 0 U; 0 Other;
Query Match 18.1%; Score 172; DB 5; Length 1296;
Best Local Similarity 51.7%; Pred. No. 4e-41;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;
QY 12 CATTATCTTTGTTGGCAGCCGCTGCTTTTGCGCTTCAATCTTTGTCATCCCCCA 71
DB 21 CATAGTTTTCCTGCTTTGTCGCGCTGCTGTAATCAATGACCTGATTTCCCA 80
QY 72 GCAGGAGTCCAGCTGTTGGAAGGCTGGGGCTTCATGCGCGCCGAGCGCGCTT 131
DB 81 GGGTAAAGCCGCGCATTTGAACGCTTGTGTAAGTACACCGCACGTTTCAAGTGGCCT 140
QY 132 GAATATTTTGAATCCCTTTATGACCGGCTGCGCTACCGCATTCGCTGAAAGAAATCC 191
DB 141 GACCTGTGTTGTTTCATTCGTGACCGAGTACCGCAAGATTCAGACCCGAGACGGGT 200
QY 192 TTTAGACGTACCCAGCTGCTGATCAACGCGCATATATGCAATTGACTGTTGACGG 251
DB 201 GGTCTCATTTCCACCGCAGGCTGTATATACCAAGAACACTGACCGTGGCATGATAT 260

QY 252 CATCATCTATTTCCAGTAACCGATCCCAACTGCGCTCATACGGTTGAGCAACTACAT 311
DB 261 CGTGTGACCTTCCAAATTCAGAACGAGCGGCCACTACGAGCGGTGACATCTACAT 320
QY 312 TATGCAATTAACCAAGCTTGGCCCAAGACGCTGCTTCCGTATCGGGCGATGAGATT 371
DB 321 CGTGTGTGAGAGATTTCTGTAGCAACCTTCGAGACCTTGTGCTGCTGATGACCT 380
QY 372 GGACAAACGTTTGAAGAGCGAGCAAAATCAACGATACGCTGCTCCGCTCGATGA 431
DB 381 GGAGAAACCTTCACTTTCAGCTGATGATTAACCGCGCTTCCGTGCGAGCTGATGC 440
QY 432 AGCCGCGGGCTTGGGTGTGAAGTCTTCGTAGCAAAATCAAGATTGTTCCGCC 491
DB 441 AGCAACCAACAAATGGGGCTTGGCATCAGCGGTGTGAATTAAGCAATTTGATTCGCC 500
QY 492 GCAGAAATCTTTCGCGCATTCAGGCAAAATTAACGCGCAAGCCGCAAAACGCGCCG 551
DB 501 ACCATCCATCCAGCATTCGATGAAAAGCATATGAAGCAGACCGTGAAGCGCGCAC 560
QY 552 TATTGCGAATTCGAAGCGCGTAATAATCGAACAAATCAACTTGCAGTGTGACGCTGA 611
DB 561 CATTTTGACGCGAAGGTTCAGCCGGAAGCCGACATCAAACTGCGAAGGTGAAGACA 620
QY 612 AGCCGAATTCAGCATTCGAGGCGAGGCTCAGGCTGCGGTCAATGCTTCAATGCGCA 671
DB 621 AGCCAGATTCCTCAGCTGAGGTGAAAGCAAGCATTCATCTGAAACGAGAAAGCAGA 680
QY 672 GAAATGCGCCGCTCAACCGCGCAAGCGCAAGCGGAATTCCTGCGCTTGTTCGCA 731
DB 681 AGCCGAAGCGATGATTCCTGCGCGCGCAAGGTGAACGCGCAGCATACCTTCAGGCGCA 740
QY 732 AGCCATGCGGAGCGCATTCGCTCAATTCGCGCGC 767
DB 741 GGTGAGGCCCGAGCATCCAAAGCTCATCGCAGC 776
RESULT 32
ADD13606
ID ADD13606 standard; DNA; 1416 BP.
XX
AC ADD13606;
XX
DT 01-JAN-2004 (first entry)
XX
DE C. glutamicum homeostasis and adaptation associated DNA SEQ ID 7.
XX
KM ds; gene; homeostasis; adaptation; environmental condition;
KM lysine production; nucleotide production; nucleoside production;
KM lipid production; fatty acid production; diol production;
KM carbohydrate production; aromatic compound production;
KM vitamin production; co-factor production; enzyme production; food;
KM animal feed; cosmetic; pharmaceutical.
XX
OS Corynebacterium glutamicum.
XX
FH Key location/Qualifiers
FT CDS 101..1398
FT /*tag= a
FT /product= "RXA00152"
XX
PN W02003040290-A2.
XX
PD 15-MAY-2003.
XX
PF 31-OCT-2002; 2002WO-EP012133.
XX
PR 05-NOV-2001; 2001DE-01054175.
XX
PA (BADT) BASF AG.
XX
PI Zeidler O, Pompejus M, Schroeder H, Kroegeer B, Klopptroge C,
PI Haberhauser G;

XX WPI: 2003-541423/51.
 DR P-PSDB; ADD13607.
 XX
 PT New nucleic acid encoding variant forms of homeostasis and adaptation
 PT proteins, useful for production of fine chemicals, specifically lysine,
 PT in microorganisms.
 XX
 PS Claim 1; SEQ ID NO 7, 336pp; German.

CC This invention describes novel *Corynebacterium glutamicum* polynucleotides
 CC and polypeptides which are associated with homeostasis and adaption to
 CC varying environmental conditions and have, at specific positions, an
 CC amino acid alteration. The products of the invention are used in a method
 CC for preparing fine chemicals in better yields, with higher productivity
 CC and/or more efficiently. Vectors that express the polypeptides of the
 CC invention are used for the production of lysine, nucleosides,
 CC nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, co-factors and enzymes. These are useful in the
 CC food, animal feed, cosmetics and pharmaceutical industries.
 CC Polynucleotides, optionally as primers and probes, can also be used for
 CC identification and classification of *C. glutamicum* and related species,
 CC e.g. for diagnosis, for genomic mapping, functional or evolutionary
 CC studies, gene manipulation and modulation of metabolic activity.

XX Sequence 1416 BP; 397 A; 415 C; 351 G; 253 T; 0 U; 0 Other;

Query Match 18.1%; Score 172; DB 10; Length 1416;
 Best Local Similarity 51.7%; Pred. No. 4,1e-41;
 Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATATCTTGTGGCAGCCGCTGCGCTTTCGCTCAATCTTGTGTCATCCCA 71
 DB 121 CATAGTTTCCGTGCTTGTGCGCGTGTGATCAATGATGCTGATGCTCCCA 180
 QY 72 GCAAGAGTCCAGCTGTGAAAAGCTCGGGCTTTCATCGCGCCCTGAGCGGCTT 131
 DB 181 GGGTAGAGCGCGCTGATTAAGCGCTTGTGATCAACCGGACCGTTTCAGTGGCT 240
 QY 132 GAATATTTGATTCCTTATGACCGCGCTGCGCTTTCATCGCGCCCTGAGCGGCTT 191
 DB 241 GACCTGCTGTTTCATTTGTTGACGAGTACCGGAGATGACACCGCTGAGCGCT 300
 QY 192 TTTAGAGTACCGAGCGCTGATCAACGCGGATTAATGCAATGATGCTGAGCG 251
 DB 301 GGTTCATTTCCACCGCAGCGCTTATTAACCAAGCAACCTGAGCGCTGATAT 360
 QY 252 CATCATCTATTTCAGATGACGATCCAACTCGCTCTATAGCTTCAGCAATCAAT 311
 DB 361 CGTGTGACCTTCCAATCAACCAACGAGCGCGCTGATCACTGAGCGCTGACATCA 420
 QY 312 TATGCAATTAACGACCTGCGCAACGAGCGCTGCGTATCGGGCTGATGAGTT 371
 DB 421 CGTGTGTGAGCAAGATTTCTTACCAACATTCGAGAGCTTGTGCTGATGACCT 480
 QY 372 GGAAGAAAGCTTGAAGAACGCGCAAAATCAACAGTACCGTCTCGCCCTGATGA 431
 DB 481 GGAAGAAAGCTTCACTTCACTGAGTGAATCAACCGCGCTCGTGGCAGCTCATGC 540
 QY 432 AGCGCGCGGGCTTGGGGTGTGAAGTCTCGCTTCAAGAAATCAAGATTTGTTCCG 491
 DB 541 AGCAACCAACCAATGGGGCTGCGCATCAACCGTGTGGAATTAAGCAATTAATCG 600
 QY 492 GCAAGAAATCTTTCGCGCAATGAGGCAAAATTAACGCGCAAGCAAGCAAGCG 551
 DB 601 ACCATTCATCAGCATGATGAGAAAGCAATGAGGCAACCGTGAAGAGCGCGCAC 660
 QY 552 TATTCGCAATCGAAGCGCGTAAATCAACAAATCAACCTTTCAGTGTGAGCGTGA 611
 DB 661 CATTTGACGCGAAGAGTCAAGCGCAAGCGCATCAAAATCGCGCAAGTGAAGCA 720
 QY 612 AGCGCAATCAACCAATCGAAGCGCGCTCAGGCTGCGCTCAATCGCTCAATGCGCA 671

DB 721 AGCCAAATGCTCTCCAGCTGAGGTTGAAAAGCAGCATTCATCTGTAAGCAGACAGA 780
 QY 672 GAAATGCGCCCGCATCAACCGCGCCAAAGGAGGAGCCGATCCCTGCGCTTGTGCCGA 731
 DB 781 AGCCAAAGCATGATCTCGCGCGCGAAGGTGAACGCCAGACGCTTCTTCAGGCGCA 840
 QY 732 AGCCAAATGCGAAGCATTCGTCGTAATTTGCGCGCG 767
 DB 841 GGTGAAGCTCGAGCATCAAAAGTCAAGCGACG 876

RESULT 33
 AAF71844
 ID AAF71844 standard; DNA; 1419 BP.
 AC AAF71844;
 XX
 DT 30-APR-2001 (first entry)
 DE *Corynebacterium glutamicum* MP protein nucleotide sequence SEQ ID NO:183.
 XX
 KW *Corynebacterium glutamicum*; metabolic pathway protein; MP protein;
 KW fine chemical production; microorganism; organic acid; nucleoside;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
 XX
 OS *Corynebacterium glutamicum*.
 XX
 PN WO200100843-A2.
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-IB000923.
 XX
 PR 25-JUN-1999; 99US-0141031P.
 PR 01-JUL-1999; 99DE-01030476.
 PR 02-JUL-1999; 99US-0142101P.
 PR 08-JUL-1999; 99DE-01031415.
 PR 08-JUL-1999; 99DE-01031418.
 PR 08-JUL-1999; 99DE-01031419.
 PR 08-JUL-1999; 99DE-01031420.
 PR 08-JUL-1999; 99DE-01031424.
 PR 08-JUL-1999; 99DE-01031428.
 PR 08-JUL-1999; 99DE-01031434.
 PR 08-JUL-1999; 99DE-01031435.
 PR 08-JUL-1999; 99DE-01031443.
 PR 08-JUL-1999; 99DE-01031457.
 PR 08-JUL-1999; 99DE-01031457.
 PR 08-JUL-1999; 99DE-01031465.
 PR 08-JUL-1999; 99DE-01031478.
 PR 08-JUL-1999; 99DE-01031510.
 PR 08-JUL-1999; 99DE-01031541.
 PR 08-JUL-1999; 99DE-01031573.
 PR 08-JUL-1999; 99DE-01031592.
 PR 08-JUL-1999; 99DE-01031632.
 PR 08-JUL-1999; 99DE-01031634.
 PR 08-JUL-1999; 99DE-01031636.
 PR 09-JUL-1999; 99DE-01032125.
 PR 09-JUL-1999; 99DE-01032126.
 PR 09-JUL-1999; 99DE-01032130.
 PR 09-JUL-1999; 99DE-01032186.
 PR 09-JUL-1999; 99DE-01032206.
 PR 09-JUL-1999; 99DE-01032227.
 PR 09-JUL-1999; 99DE-01032228.
 PR 09-JUL-1999; 99DE-01032229.
 PR 09-JUL-1999; 99DE-0103230.
 PR 14-JUL-1999; 99DE-01032822.
 PR 14-JUL-1999; 99DE-01032826.
 PR 14-JUL-1999; 99DE-01032928.
 PR 14-JUL-1999; 99DE-01033004.
 PR 14-JUL-1999; 99DE-01033005.
 PR 14-JUL-1999; 99DE-01033006.

PR 12-AUG-1999; 99US-0148613P.
PR 27-AUG-1999; 99DE-01040764.
PR 27-AUG-1999; 99DE-01040765.
PR 27-AUG-1999; 99DE-01040766.
PR 31-AUG-1999; 99DE-01040832.
PR 31-AUG-1999; 99DE-01041378.
PR 31-AUG-1999; 99DE-01041379.
PR 31-AUG-1999; 99DE-01041380.
PR 31-AUG-1999; 99DE-01041394.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042077.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042124.
PR 03-SEP-1999; 99DE-01042129.
PR 09-MAR-2000; 2000US-0187970P.

XX (BADI) BASF AG.

PI Pompeius M, Kroegeer B, Schroeder H, Zelder O, Habernauer G;

DR WPI; 2001-137957/14.

XX P-PSDB; AAB79725.

PT Nucleic acids from *Corynebacterium glutamicum* encoding metabolic pathway
proteins, useful for producing fine chemicals in microorganisms,
including organic acids, nonproteinogenic amino acids, and purine and
pyrimidine bases.

PS Claim 3; Page 422-424; 17370p; English.

XX AAF1753 to AAF72330 encode the *Corynebacterium glutamicum* metabolic
pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP
nucleic acids are useful for the production of fine chemicals in
microorganisms, including organic acids, nonproteinogenic amino acids,
purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated
and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,
vitamins, cofactors, polyketides and enzymes

XX Sequence 1419 BP; 397 A; 416 C; 353 G; 253 T; 0 U; 0 Other;

Query Match 18.1%; Score 172; DB 4; Length 1419;

Best Local Similarity 51.7%; Pred. No. 4,1e-41;

Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATTATCTGTGTGGAGCGCGTTCGCTTTCGCTTCAATCCTTGTGTCATCCCA 71
DB 121 CATAGTTTTCGCGCTTGTGCGCGTGTGTGATCAAGTCAAGCCGATGCCCA 180
QY 72 GCAGGAAGTCCAGCTTTCGAAAGCGTGGCGCTTTCATGCGCCCTGACGCGGTTT 131
DB 181 GGGTGAACCGCGCTTGAAGCGCTTGTGTGATCAACCGCGCTTTCAGGCGCT 240
QY 132 GAATATTTTGAATCCTTATGACCGGCGCTTACCGCATTTGCTGAAAGAAATCC 191
DB 241 GACCTGCTGTTTCATTCGTGACGAGTACGCGCAAGATGACACCCGTGAGCGCT 300
QY 192 TTTAGACGTACCAAGCTGCTGATCAGCGCGCATTAATGCAATGACTGTTGACG 251
DB 301 GGTGTCATTTCCACGCGAGCGGTATTATACCAAGAACGACGCGGCGCATGATAT 360
QY 252 CATCATTTATTTCCAGTACCGATCCAAATGCGCTTCATACGGTTGAGCACTACAT 311
DB 361 CGTGTGACCTTCCAAATCAAGAACGAGCGCGCATCATCGCGCTGCACTACAT 420
QY 312 TATGCAATTAACCGCTTGGCCAAAGACGCGCTTCCGTTATCGGCGGATGAGATT 371
DB 421 CGTGTGTGAGACGATTTCTGTAGCAACCTTGAGACGTTGCGGTGCGATGACCT 480

QY 372 GCACAAACGTTTGAGAGACGACGAATATCAAGATACCGTGTCTCCGCCCTGATGA 431
DB 481 GGAAGAAACCTTCACTTACGTGACGTATCAACCGCGCTTCGTTGCGAGCTGATGC 540
QY 432 AGCGCCGGGGCTTGGGGTGAAGTCTCTCGTTAGCAATTCAGATTTGTTCCGCC 491
DB 541 AGCAACCAACAAATGGGGCTGCGCATAGCGTGTGAACTAAAGCAATTTGATCCGC 600
QY 492 GCAAGAAATCTTCCGCGCATATGACAGGCAATTAACGCCGAACGCAAAACGCGCCG 551
DB 601 ACATTCATTCAGCAATGATGAGAAAGCAATGAGGACACCTGAAAAGCGGCCAC 660
QY 552 TATTCGCAATTCGAGGCGGTAAATTCGAACAAATCACTTGCCAGTGTCAAGCTGA 611
DB 661 CATTTTGACCCGAGAGGTACAGCGGAAGCGACATCAAACTGCGCGAAGGTGAAGCA 720
QY 612 AGCGGAATTCGAATTCGGAAGCGGAGCTTCAGGCTCGGTTCAATGTTCCATCCGA 671
DB 721 AGCCAAAGTCTTCCAAAGCTGAGGGTGAAGAACAGCATTCATCTGAAACGAGAAACGA 780
QY 672 GAAATCGCCCGCATCAACCGCGCAAGGCGGAAGCGGAATCCCTGCGCTTGTTCGCA 731
DB 781 AGCCCAAGCATGATCTTCGCGCGCGGAGGAGTGAACGCGCAGCAGCTTCCAGGCGCA 840
QY 732 AGCCAAATCCGAGCCATTCGCTCAATTTGCCGCGC 767
DB 841 GGTGTAAGCCCGAGCAATCCAAAGGTCAACGACGC 876

RESULT 34

AAAF71207 standard; DNA; 1419 BP.

XX AAF71207;

AC 30-APR-2001 (first entry)

DT *Corynebacterium glutamicum* HA protein nucleotide sequence SEQ ID NO:139.

DE *Corynebacterium glutamicum* HA protein nucleotide sequence SEQ ID NO:139.
XX *Corynebacterium glutamicum*; homeostasis; adaptation; HA protein;
fine chemical production; organic acid; proteinogenic amino acid;
nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
diagnosis; *Corynebacterium* diphtheriae; genetic engineering;
KW *Brevibacterium*; environmental condition; de.

OS *Corynebacterium glutamicum*.

PN MO200100842-A2.

PD 04-JAN-2001.

XX 23-JUN-2000; 2000WO-IB000911.

PF 25-JUN-1999; 99US-0141031P.

XX 08-JUL-1999; 99DE-01031636.

PR 09-JUL-1999; 99DE-01032125.

PR 09-JUL-1999; 99DE-01032126.

PR 09-JUL-1999; 99DE-01032127.

PR 09-JUL-1999; 99DE-01032128.

PR 09-JUL-1999; 99DE-01032226.

PR 09-JUL-1999; 99DE-01032920.

PR 14-JUL-1999; 99DE-01032922.

PR 14-JUL-1999; 99DE-01032924.

PR 14-JUL-1999; 99DE-01032930.

PR 14-JUL-1999; 99DE-01032935.

PR 14-JUL-1999; 99DE-01032973.

PR 14-JUL-1999; 99DE-01033002.

PR 14-JUL-1999; 99DE-01033003.

CC production of fine chemicals, preferably amino acids and specifically
CC lysine, but more generally nucleosides, nucleosides, lipids, fatty acids,
CC diols, carbohydrates, aromatic compounds, vitamins, co-factors and
CC enzymes, useful in the food, animal feed, cosmetics and pharmaceutical
CC industries. The polynucleotides of the invention, optionally as primers
CC and probes, can also be used for identification and classification of C.
CC glutamicum and related species, e.g. for diagnosis, for genomic mapping,
CC functional or evolutionary studies, gene manipulation and modulation of
CC metabolic activity. Cells containing the products of the invention may
CC produce fine chemicals in improved yields, with higher productivity
CC and/or more efficiently.

XX Sequence 1426 BP; 401 A; 418 C; 354 G; 253 T; 0 U; 0 Other;

Query Match 18.1%; Score 172; DB 10; Length 1426;

Best Local Similarity 51.7%; Pred. No. 4,1e-41;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATATCTTTGTTGGACGCGCTGCGCTTTGCGCTTCAATCTTTGTGTCATCCCCCA 71
DB 121 CATAGTTTTCCTGCTCTTTGTGCGCGTGTGATCAAGTCCATAGCCCTGATTCGCCA 180
QY 72 GCAGGAAGTCCACCTTTGCGAAAGGCTGCGGCTTTCATGCGCGCTGACGCGCGTTT 131
DB 181 GGGTGAAGCGCGCTGATTTGAAGCGCTTGATGATACACCGCGCTTTCAGTGCGCT 240
QY 132 GAATATTTTGTATTCCTTTATGACGCGCGTGCCTACGCGCATGCTGCTGAAGAATCCC 191
DB 241 GACCGTGTGCTGCTTCAATCTTGTGATCGAGTACCGCGAAGATCGACACCGCGCGGT 300
QY 192 TTTAGACGTACCGACGAGTGTGATCAACGCGCGATTAATGCAATTGACTGTTGACGG 251
DB 301 GGTCTCATTTCCACGCGAGGCTGTTATTAACCAAGACAACTGACCGTGCGCATGATAT 360
QY 252 CATCATTTATTTCCAGTAACCGATCCCAAACTGCGCTCATGCGTGTGAGAACTTAACT 311
DB 361 CGTGTGACCTTCAATCAATCAAGAACGAGCGCGCTATTAACGCGCTGAGAACTTAACT 420
QY 312 TATGCAATTTACCAAGTGTGCGCAACGCGTGTGCTGTTATCGGCGCTGATGAACTT 371
DB 421 CGTGTGTGTGAGCAGATTTCTGTAGCAACTTGTGAGACGTTGTGCGGTGATACCTT 480
QY 372 GACCAAAAAGTTGAAAGACGCGCAAAATCAACAGTACCGTGTCTCGCGCTGATGTA 431
DB 481 GGAAGAAAACCTCATTGACGTGATCAACGCGCGCTCGTGCGAGCTGATGATG 540
QY 432 AGCGCGCGCGGCTGTGAGTGAAGTCTCGCTTACGAAATCAAGATTTGTTGCGCG 491
DB 541 AGCAACCAACCAATGCGCGCTGTGCGATGACCGTGTGAACTTAAAGGCAATTTGATC 600
QY 492 GCAAGAAATCTCTTCCGCAATGACGCAAAATTAACCGCGCAACCGCAAAACGCGCG 551
DB 601 ACCATTCATCCGCAATGATGAGAAAGCAATGAGGCAACCGTGAAGAGCGCGCAC 660
QY 552 TATTGCGCAATCGAAGCGCGTAAATGCAACCAATCAACTTGTGCTGACGCTGA 611
DB 661 CATTTGACCGGAGAGGTCAAGCGGAAAGCAATCAAAATGCGGAAAGTGAAGAA 720
QY 612 AGCGCAATTCGAAGTGTGAGGAGGCTGAGGCTGCGGTCAATGCTGCAATGCGCG 671
DB 721 AGCGCAAGTCTTCAGGTGAGGAGTGAAGAACGCAATTCATCTGAAACGCAAGAG 780
QY 672 GAAATTCGCGCGCATCAACGCGCGCAAGAGCGCAAGCGCAATTCGCGCTTGTGCGGA 731
DB 781 AGCGCAAGGATGATCTGCGCGCGCGAGAGTGAAGCGCGCAAGCGCTTACCTTCA 840
QY 732 AGCGCAATTCGCAAGCGCATCTGCAATTTGCGCGCG 767
DB 841 GGGTGAAGCGCGGCAATTCAAAAGTCAAGCGCAG 876

RESULT 36
AAH68529/c

ID AAH68529 standard; DNA; 349980 BP.

XX AAH68529;

XX 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 7064.

XX Corynebacterium; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EP1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-00127688.

XX 16-DEC-1999; 99JP-00377484.

XX 07-APR-2000; 2000JP-00159162.

XX 03-AUG-2000; 2000JP-00280988.

XX (KIOWA) KIOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

XX Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI, 2001-376931/40.

XX Disclosure: SEQ ID NO 7064; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

XX sequences from the Corynebacterium glutamicum. These

XX are useful for identifying the mutation point of a gene derived from a

XX mutant of corynebacterium, measuring expression amount and analyzing

XX the expression profile or expression pattern of a gene derived from

XX Corynebacterium, and identifying a homologue of a gene derived from

XX corynebacterium. Corynebacterium bacteria are useful for producing amino

XX acids, nucleic acids, vitamins, saccharides and organic acids,

XX particularly L-lysine. The present sequence is a nucleic acid described

XX in the exemplification of the invention. Note: The sequence data for this

XX patent did not form part of the printed specification, but was obtained

XX in electronic format directly from the European Patent Office

XX Sequence 349980 BP; 82466 A; 95954 C; 90516 G; 81044 T; 0 U; 0 Other;

XX Query Match 18.1%; Score 172; DB 5; Length 349980;

XX Best Local Similarity 51.7%; Pred. No. 5.1e-40;

XX Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 12 CATATCTTTGTTGGACGCGCTGCGCTTTGCGCTTCAATCTTTGTGTCATCCCCCA 71

DB 119596 CATAGTTTTCCTGCTCTTTGTGCGCGTGTGATCAAGTCCATAGCCCTGATTCGCCA 119537

QY 72 GCAGGAAGTCCACGTTGCGAAAGGCTGCGGCTTTTCATGCGCGCTGACGCGGTTT 131

DB 119536 GGGTGAAGCGCGCTGATTTGAAGCGCTTGATGATACACCGCGACCGTTTACGCGGCT 119477

QY 132 GAATATTTTGTATTCCTTTATGACGCGGCTGCGCTTACCGCATTCGCTGAAGAATCCC 191

DB 119476 GACCGTGTGCTGCTTATTCGTCGACGAGTACGCAAGATGCAACCGCTGACGCGGT 119417

QY 192 TTTAGACGTACCGACGAGTGTGATCAACGCGCGATTAATGCAATTTGATGTCGCG 251

DB 119416 GGTCTCATTTCCACGCGAGGCTGTTATTTACCAAGACAACTGACCGGTGCGCATGATAT 119357

QY 252 CATCATTTATTTCCAGTAACCGATTCCAAATTCGCTCATGCGTTGAGCAACTATCAT 311

Db 119356 CGTGTGACCTTCCAAATCAAGAACGACGAGCGCCCATCTAAGCGGTGACACATACAT 119297
 QY 312 TATGGCAATTACCCAGCTTGCCCAACGACGCTGCGTTCCGTTATCGGCGTATGAGTT 371
 Db 119296 CCGTGGTGAGACAGATTTCTGTAGCAACACTTGCAGACGTTGTCGGTGCATGACCT 119237
 QY 372 GGAAGAAAGTTTGAAGAACGAGCAAGAAATCAACAGTACCGTTCGCGCCCTGATGA 431
 Db 119236 GGAAGAAAGCTTCACTTCACTGACGTCATCAACCGCCGCTTCGTCGAGCTCATGTC 119177
 QY 432 AGCCGCGCGGGCTTGGGCTGTGTAAGTCTCGCTTCAAGAAATCAAGATTTGGTCCGC 491
 Db 119176 AGCAACCAACCAATGGGCGCTGCGCATCAGCGCTGTGAACTTAAAGCAATGATCCGC 119117
 QY 492 GCAAGAAATCTTTCGCGCAATGACGACCAATTAACCGCCGAAACGCGAAACGCGCCG 551
 Db 119116 ACCATCATCAAGCATCATGATGAAAGAGATGAAAGCAGACCGTGAAGGCGCCAC 119057
 QY 552 TATGCGCAATCGAAGGCGCTTAAATTCGAACAAATCAACTTGCAGTGTCAAGCTGA 611
 Db 119056 CATTTTGACCGAGAAAGTCAAGCGCGACGACCATCAAACTGCGAAGGTGAAGCA 118997
 QY 612 AGCCGAATTCACCAATTCGAAAGCGAGGCTCAAGCTGCGTCAATGCTCCATGCCGA 671
 Db 118996 AGCAACGATCTCTCAAGCTGAGGCTGAAAGACGATCATCTGAAGCAGAGACGA 118937
 QY 672 GAAATCGCCCGCATCAACCGCGCCCAAGGCGAAGGGAATCCCTGCGCTTGTGCCGA 731
 Db 118936 AGCCCAAGGATATCTCTGCGCGCCGAAAGGTGAACGCGACGCTACTCCAGCGCA 118877
 QY 732 AGCCAAATGCCGAAGCCATCGCTCAAAATTTGCGCGCG 767
 Db 118876 GGGTGAAGCCCGAGCAATCCAAAGGTCAACGACG 118841

RESULT 37
 ABL05449
 ID ABL05449 standard; cDNA; 1153 BP.
 XX
 AC ABL05449;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10829.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB; ABB61346.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Claim 1; SEQ ID NO 10829; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB87737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://pub/published_pcr_sequences

XX Sequence 1153 BP; 298 A; 297 C; 333 G; 225 T; 0 U; 0 Other;

SQ Query Match 17.5%; Score 165.6; DB 4; Length 1153;

Best Local Similarity 51.8%; Pred. No. 3.2e-39;

Matches 427; Conservative 0; Mismatches 364; Indels 33; Gaps 1;

QY 56 TTGTGTCATCCCGCAGAGAAAGTCAAGTGTGAAAGGCTCGGGGTTTCCATCCG 115
 Db 152 TTATGTTTGTGCCAGCAAGAGCGCTGGGTGTGAGCGCATGCGGCGCTTTCACAGGA 211
 QY 116 CCTGACGCGCGTTGAAATATTTGATTCCTTTATGACCGCGCTACCGCAAT 175
 Db 212 TTTTGACCCCGACTCAACATATATGTCCTGGTGGCGAACAATCAATACGTCCAGA 271
 QY 176 CGCTGAAGAAATCCCTTTAGACGTACCAAGCGACGATGTCATCAAGCGCATTAACGC 235
 Db 272 GCTTAAGAAATTCCTCATAGTGTGCCAAACAGCGCTATTACCTCCGACAACTGA 331
 QY 236 AATTGACTGTGACGCGATCATCTATTTCCAGTAACGATCCAACTCGCTCATACG 295
 Db 332 CCTGAGATGACGCGCGTCTCTACTTCCGATCATGATCGTAAAGCTGTACG 391
 QY 296 GTTCAAGCACTACATATATGAGCAATTAACCACTTCCCAACGACGCTGCTCCGTTA 355
 Db 392 GCGTGAAGATCCGAGTTCGCGATTAACAACATGCGCCACGACGATGAATGAGAC 451
 QY 356 TCGGGCGTATGAGTTGACAAAGCTTTGAAGAACGACGCAAAATCAACAGTACCGTGC 415
 Db 452 TGGGCAAGTATTCATGACAGAGTCTTCGCGAAAGGAGATCCTCAACGTACAGATCG 511
 QY 416 TCTCCGCTTCATGAAAGCGCGCGCTTGGGGTGTGAAAGTCTTCGTTACGAATCA 475
 Db 512 TCGATCGATCAACAAGCGCAGCGGCGTGGGATCGCTGTGCGATACGAGATCG 571
 QY 476 AGAATTTGTTCCGCGCAAGAAATCTTCGCGCAATGAGCAACAATTAACCGCGAAC 535
 Db 572 GTGATATTCGACTGCCACAGGTTTCAGAGCGATGCAAGTGAAGGCCGAGC 631
 QY 536 GCGAAAGAGCGCCGATTTGCGAATCGAAGCGGTAAATTCGAACAATCAACTTG 595
 Db 632 GCGAAAGCGAGCCGCTATTTGAAATCGA----- 662
 QY 596 CCAATGTCAGCGTGAAGCGCAATTCACAATTCGAAGCGAGGCTCAGGTCGCGTCA 655
 Db 663 -----GGGTGTTGCGAGGCGCAATTCACATGCGGCAAGCGGAAGTCTAAGATTTC 718
 QY 656 ATGCGTCAATGCGGAAATTCGCCCGCATCAACCGCCCAAGCGCAAGCGGAATCCC 715
 Db 719 TAGCTTCGAGCGGAGCGCGCAGAGCATCAATGAAGCAGCGGAGGCGGCTGCCA 778
 QY 716 TCGGCTTGTGCGGAAGCATGCGGAAGCATCGCAATTAATGCGCGCGCTTCAAA 775
 Db 779 TTATAGCCGTGGGATGTCAGAGCCGCAAGTCTATCGCCATAGCAATCTTATCCC 838
 QY 776 CCCAAGCGCGGCGATGCGGTCAATCTGAAGATTGCGGACAAATACGTAGCGCGTTCA 835
 Db 839 ACTGTAGTGAAGATGCTGTGCTCAGCGTGCAGAGATGATGAGGCTTCA 898
 QY 836 ACAATTTGCCAAGAAAGCAATAGCTGATTAATGCGCGCAAT 879
 Db 899 AGAAGCTGCCAAGAGCAATTAACCATGATCTTGCCCTCGAAT 942

RESULT 38
ADJ39266 standard; cDNA; 1218 BP.
AC ADJ39266;
DT 06-MAY-2004 (first entry)
XX
DE Plant cDNA #266.
XX
XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
XX soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
XX maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
XX stress tolerance; salt tolerance; cold tolerance; drought tolerance;
XX plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX antifungal.
XX
OS Eukaryota.
XX
XX
XX US2004016025-A1.
XX
XX
XX 22-JAN-2004.
XX
XX
XX 26-SEP-2002; 2002US-00260238.
XX
XX
XX 26-SEP-2001; 2001US-0325277P.
XX 26-SEP-2001; 2001US-0325448P.
XX 04-APR-2002; 2002US-0370620P.
XX
XX
XX (BUDWORTH P.
XX (MOUGHAMER T.
XX (BRIGGS S P.
XX (COOPER B.
XX (GLAZEBROOK J.
XX (GOLF S A.
XX (KATAKATA KATAGIRI F.
XX (KREPS J.
XX (PROVART N.
XX (RICK D.
XX (ZHU T.
XX
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J,
XX Golf SA, Katagiri F, Kreps J, Provart N, Rieke D, Zhu T,
XX
XX WPI: 2004-190374/18.
XX
XX
XX New rice promoter, useful for manipulating crop plants to alter or
XX improve phenotypic characteristics, e.g. produce large quantities of oil
XX or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX or high nutritional value.
XX
XX
XX Claim 68; SEQ ID NO 266; 230bp; English.
XX
XX
XX The invention relates to plant nucleotide sequences that direct seed-,
XX leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX or constitutive transcription of an operatively linked nucleic acid
XX segment. The invention also relates to a method for augmenting a plant
XX genome and a method of identifying a gene, where its expression is
XX altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX encode are useful for manipulating crop plants to alter or improve
XX phenotypic characteristics, to produce large quantities of oil or
XX proteins, to incur resistance to insecticides, viruses or fungi, and to
XX incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX have a high nutritional value with reduced apical dominance or dwarfism,
XX early flowering or altered metabolic pathways. This sequence represents a
XX plant nucleic acid of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification but was obtained in
XX electronic format directly from USPTO at seqdata.uspto.gov/Sequence.html.
XX
XX Sequence 1218 BP; 289 A; 348 C; 329 G; 252 T; 0 U; 0 Other;

Query Match 16.9%; Score 160.2; DB 12; Length 1218;
Best Local Similarity 53.4%; Pred. No. 1.4e-37;
Matches 336; Conservative 0; Mismatches 293; Indels 0; Gaps 0;
OY 60 CGTCATCCCCCAGAGAAAGTCACGTTGCGAAAGCGCTGGGCGTTCCATCGCCGCT 119
DB 258 CATCGTCGCGAGAGAAAGCGCTTCGTGTGTGAGACGGCTCGGCAAGTACGACAGAGCGCT 317
OY 120 GACGCGCGGTTGAAATTTTGTGATTCCTTATGACCGCGTGCCTACCGCGCATGGCT 179
DB 318 CGGCTCGGAGTCCACGCTGCTGCTCCCTGCTGACCGCATCGCTACGTCACGCTGCT 377
OY 180 GAAAGAAATCCCTTTAGACGTACCCAGCAGGTGCTGATCAGCGCCATATATAGCAATT 239
DB 378 CAAGAGAGAGGCGCATCCCGCATCCCGACAGTCGCGCATATCAAGAGCAACGCTCCAT 437
OY 240 GACTGTGACGCGCATCATCTATTTTCCAAAGTACCGATCCCAATCGCTCATACGTTTC 299
DB 438 CCAGATCGACGCGCTCCTCTACGTCAAGATTGTGATCCCTACCTTCTCTATGTGTGT 497
OY 300 GAGCAACTACATTAATGGAATTAACCGCTTGGCCCAAGACGCGTGGCTTCGTTATCGG 359
DB 498 GAGATATCAATTTTGTGAGTCATACGCTTGCCTCCCAACATATGAGAGTACGCTTGG 557
OY 360 GCGTATGAGATTGGAACAACAGTTTGAAGACGCGACGAATCAACAGTACGCTCTC 419
DB 558 AAAGATTACGCTATACAAAGATCTTTGAGAGAGGAGATACATTAATGAGCAATTTGTAG 617
OY 420 CGCCCTCGATGAGCGCGCGGCGCTTGGGCTGTGAAAGTCTCCGTTACGAATCAAGGA 479
DB 618 GTCCATTATAGAGCTGCACTGATGGGACTGAAATGCTCCGTTATGAGATCAAGGA 677
OY 480 TTTGGTCCCGCGGAAGAAATCCTTCGCGCAATGAGCAACAAATTAACCGCGAAGCGGA 539
DB 678 TATATCTCCGCGACGTGTGTTAAGTGGCTATGAGATGTCAGACAGACGAAGAGAA 737
OY 540 AAAAGCGCCCGCTATTTGCGCATCCGAAGCGCGTAAATCGAACAATTCATTGCGCAG 599
DB 738 AAAGGTGCCCAATTCCTGTAATCAGAAAGTGCTATGTGATCAGGAAATTCGCGCAA 797
OY 600 TGTGACGCTGAGACCGCAATTCACCAATCCGAAGGCGAGGCTCAGGCTGGCTCAATGC 659
DB 798 GGGTGAGGCTGACCAATTCCTGCAAAAGTCTGAAGCAACTGCTGAGGAATCAGATTGGT 857
OY 660 GTCCATGCGGAGAAATTCGCGCGCATCA 688
DB 858 CTGTAGGCGCATGAGAGCAAGGAGCA 886
RESULT 39
ADN97415 standard; DNA; 1071 BP.
XX
XX ADN97415;
XX
XX
XX 29-JUL-2004 (first entry)
XX
XX
XX Human SLP2 DNA for pain treatment.
XX
XX
XX ds; gene; analgesic; gene therapy; neuronal mechano-transduction;
XX stomatin domain; current; voltage; plasma membrane; neuron; pain.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..1071
XX /*tag= a
XX
XX W02004040299-A2.
XX
XX 13-MAY-2004.
XX

30-OCT-2003; 2003MO-BP012084.
 30-OCT-2002; 2002EP-00024474.
 30-OCT-2002; 2002US-0422098P.
 (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 Lewin G, Heppenstall P, Eilers A,
 WPI; 2004-376269/35.
 P-PSDB; ADN97416.
 Identifying a compound capable of inhibiting the mechano-transduction of
 a neuron for treating pain by measuring the current or voltage at the
 plasma membrane of the cell contacted with the candidate compound.
 Disclosure; SEQ ID NO 13; 100pp; English.
 The invention relates to a method of identifying inhibitors of neuronal
 mechano-transduction by: (a) providing a cell over expressing a
 polypeptide comprising stomatin domain-containing proteins; (b)
 contacting the cell with a candidate compound; (c) measuring the current
 or voltage at the plasma membrane of the cell; and (d) identifying the
 candidate compound as an inhibitor of mechano-transduction if the current
 or voltage measured is altered in comparison to a control. The
 polynucleotide encoding the stomatin domain-containing protein, the
 polypeptide encoded by the polynucleotide, the cells over expressing the
 polypeptide comprising stomatin domain-containing proteins or the system
 is useful in identifying a compound capable of inhibiting the mechano-
 transduction of a neuron for preparing a composition for treating pain.
 This sequence corresponds to the human SLP2 DNA used in the invention.
 Sequence 1071 BP; 252 A; 293 C; 316 G; 210 T; 0 U; 0 Other;
 Query Match 16.4%; Score 155.6; DB 12; Length 1071;
 Best Local Similarity 50.6%; Pred No. 3.3e-36;
 Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;
 62 TCATCCCCCAGAGGAAAGTCAAGTGTGAAAGGCTCGGGGCTTTCATCGCGCCCTGA 121
 119 TCGTGGCGGAGAGGAGGCTGGGTGTGAGAGAAATGGGCGGATTCACCGGATCTCG 178
 122 CGGCGGTTTGAATATTTGATTCCTTATGACCGCGCTGCTACCCGCTATCGCTGA 181
 179 AACCTGGTTTGAACATCTTCATCCCTGTGTAGACCGAATCCGATATGTGCGAGATCTTA 238
 182 AAGAAATCCTTTAGAGGTACCGAGCGAGGTCTGATCAAGCGGATTAATAGCAATTGA 241
 239 AGGAAATTTTCATCAACGCTGAGCAAGTGGCTGTGACTCTTCGACAAATGTAATCTTCG 298
 242 CTGTGACCGCATCATCTATTTTCAGATTAACGATCCCAACTCGCTCATAGCTTGA 301
 299 AATATGATGAGATGCTTTACCTGCGATCATGAGACCTTAACAAGGATGAGGTG 358
 302 GCAACTACATTTATGCAATTTACCGACTTGGCCAAAGAGCGCTTCCGTTATGCGG 361
 359 AGGACCTGAGTATGCGCTACCGCACTAGCTCAACCAACATGAGATGAGAGCTGGGA 418
 362 GATATGAGTTGACAAAGCTTTGAAAGACGAGCAAAATCAACATACGCTGCTCG 421
 419 AACTCTCTTGACAAAGTCTTCGGGAAAGGAGTCCCTGAAATGCGAGATTTGAGATG 478
 422 CCCTGATGAAGCGCGCGGGCTTGGGCTGTGAAAGTCTCCGTTAGCAATCAAGATT 481
 479 CCAATCAACAGCTGCTGACTGTGGGATTCGCGCTCCGTTATGAGATCAAGATTA 538
 482 TGGTCCGCGCAAGAAATCTTTCGCGCAATGACGACCAATTAACCGCGCAACCGGAA 541
 539 TCCATGTGCGACCCCGGGTGAAGAGATCTATGCAAGATGACGAGGACGAGCGCGGA 598
 542 AACGGCCCGTATTTGCGGATCGGAAGCGGCTAAATTCAGAAACAACTTGGCCAGTG 601
 599 AACGGCCCAAGTGTGAGATCTGA-----GG 625

602 GTACGCGTGAAGCCGAAATTCACAAATCCGAGGCGAGCTCAGGCTCGCTCAATGCGT 661
 626 GAGCCGAGAGTCTGGCCATCAATGTGGGAGAGAGAGAAACAGGCCCAAGATCTCGGCT 685
 662 CCAATGCGGAGAAATATGCGCCGATCAACCGCGCAAGCGGAAATCCCTGCGCC 721
 686 CCGAAGGAGAAAGGCTGAACAGATTAATCAAGGACGAGAGAGGCCAGTGCAGTTCTGG 745
 722 TTGTTGCGGAAAGCCATGCGGAGCATTCCTCAATTTGCGCGCCCTTCAAAACCCAG 781
 746 CGAAGCCCAAGGCTTAAGCTGAAGCTATTCAATCTGCTGACGCTGACACAACTTA 805
 782 GCGGGGCGGATGCGGCTCAATCTGAAGATTGGGGAACAAATAGTAGCCGCTTCAACATTC 841
 806 ATGAGATGACAGACACTTCACTGACTGTGGCCGAGACATATGTACGCCGCTTCCCAAC 865
 842 TTGCCAAGAAAGCAATAGCTGATTATGCGCGCAATGTTGCCGACATCGGACGCTGA 901
 866 TGCCCAAGAGATCCCAACACTATCTTACTGCTCCCAACCGTGGGAGATGACACGATGG 925
 902 TTTCTGCGGCGATG 915
 926 TGCTCAAGGCGCATG 939
 RESULT 40
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 ID AAH13961 standard; cDNA; 1244 BP.
 XX
 AC AAH13961;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:11009.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99UP-00248036.
 XX
 PR 27-AUG-1999; 99UP-00300253.
 XX
 PR 11-JAN-2000; 2000UP-00118776.
 XX
 PR 02-MAY-2000; 2000UP-00183767.
 XX
 PR 09-JUN-2000; 2000UP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 XX
 PT length cDNAs defined in the specification, and for the detection and/or
 XX
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 XX
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 11009; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification, where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH016 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

Sequence 1244 BP; 284 A; 327 C; 368 G; 265 T; 0 U; 0 Other;

Query Match 16.4%; Score 155.6; DB 4; Length 1244;
Best Local Similarity 50.6%; Pred. No. 3.6e-36;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

62 TCATCCCCAGAGAGATCCAGCTGTGCAAAAGGCTCGGCGTTTCATCGCGCTGA 121
153 TCGTCCCGCAGAGAGGCTGGGTGTGAGCAATGGGCGATTCACCGGATCTTG 212
122 CGGCGGTTGAATTTTGAATTCCTTATCGACGGGCTGACCGCATTCGCTGA 181
213 AGCTGTGTTGAACATCTCATCTCTGTGTAGACCGGATCGATATGTGCAAGTCTCA 272
182 AAGAAATCCCTTGAACGTACACAGCAGTCTGCATCAGCGCGATTAATAGCAATTTGA 241
273 AGGAAATGTGATCAACGTGCTGAGCAGTGGCTGTGACTCTGCAATGAATCTGTC 332
242 CTGTGACGCGATCATTAATTTCAAGTAACCGATCCAAACTGCTCTATACGTTTGA 301
333 AAATGATGAGATCTTTACCTGCGCATCATGAGACCTTACAAAGCAAGCTACGGTGTG 392
302 GCAATCATATATGCAATTTCCGAGCTTGCCTCAAGACGCTGCTCCGTTATCGGGC 361
393 AGGACCTGAGATGCGGTCAACCGCTAGCTCAAAACAACATGATGAGAGCTGGCA 452
362 GTATGAGTTGAGCAAAAGTTTGAAGACGCAAGCAATCAACAGTACCGTCTCTCG 421
453 AACTCTCTGAGCAAAAGTTTCCGGGAACGGAGTCCCTGATGCCAGCATTTGTGATG 512
422 CCTTGAATGAAGCCGCGGCTTGGGTGTGAAGTCTCTCCGTTACGAAATCAAGATT 481
513 CCATCAACCAAGCTGCTGATGCTGGGTATCCGCTGCTCGTTATGATCAAGGATTA 572
482 TGGTTCCGCGCAAGAAATCTTCCGCGCATGCAAGCAAAATTACCGCGCAAGCGGAA 541
573 TCCATGTGCAACCCGCGGTGAAGAGTCTATGCAATGAGTGAGGCAAGCGCGGA 632
542 AACGCGCCGATTTGCGGATCCGAATCCGAAGGCCGTAATCAACCAATCAACTTGGCA 601
633 AACGGGCAAGTTCTAGAGTGA-----GG 659
602 GTCAAGCTGAAGCCGAAATCCCAATCCGAATCCGAAGGCTGAGGCTGCGGTCAATGCGT 661
660 GGAACCCGAGAGTGGGCAATCATGTGCAAGGAGGAAAGAAACAGGCCCAAGATCCCTGGCCT 719
662 CCAATGCGGAGAAATCCGCGCATCAACCGCGCAAGGCGAAGCGGAATCCCTGCGCC 721
720 CCGAAGCAAGAAAGGCTGAACAGATTAATCAAGGCAAGGAGGCAAGTCAAGTCTGCG 779
722 TTGTTCCGAAGCCATGCGGAGCATCCGTCATTAATTTGCGCGCTTCAAAACCAAG 781
780 CGAAGGCCAAGGCTTAAGCTGAAGCTATTGCAATCTGCTGCACTTGAACAACATA 839
782 GCGGGCGGATGCGGTCAATCTGAAGATTGCGGAACAAATACGTAGCCGCTTCAACATC 841
840 ATGGAATGACAGAGCTTCACTGACTGTGCGCAAGCATATGTCAAGCGGTTTCCAAAC 899

Qy 842 TTGCCAAGAAAGCAATACGCTGATTAATGCCCCCAATGTTGCCACATCGGACGCTGA 901
Db 900 TGGCCAAAGACTCCAAACATTAATCTTACTGCTCCAAACCTGGGAGATGTACACAGATGG 959
Qy 902 TTCTGCGCGATG 915
Db 960 TGGCTCAGGCGATG 973

Search completed: August 13, 2005, 23:29:22
Job time : 624 secs

3

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 22:22:31 ; Search time 207 Seconds
(without alignment)

7493.673 Million cell updates/sec

Title: US-10-018-470A-16

Perfect score: 948
Sequence: 1 atggaatttcattcattctt.....gcagcaaaccccaataa 948Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 8181335 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	18.1	1419	4	US-09-602-777A-139
2	155.2	16.4	1188	1	US-08-781-562-2
3	153.2	16.2	4403765	3	US-09-103-840A-2
4	153.2	16.2	4411529	3	US-09-103-840A-1
5	141.4	14.9	963	4	US-09-543-681A-2806
6	130.2	13.7	951	4	US-09-489-039A-6125
7	113	11.9	1107	4	US-09-902-540-4035
8	113	11.9	24986	4	US-09-902-540-1200
9	104.2	11.0	840	4	US-09-902-540-6837
10	104.2	11.0	4026	4	US-09-328-352-126
11	96	10.1	870	4	US-09-540-236-1751
12	84.6	8.9	885	4	US-09-540-236-1751
13	84.6	8.9	100848	4	US-09-540-236-1751
14	77	8.1	558	4	US-09-252-991A-5885
15	70.4	7.4	532	4	US-09-621-976-1043
16	64.8	6.8	840	4	US-09-248-796A-2756
17	59	6.2	546	4	US-09-252-991A-5903
18	58.8	6.2	546	4	US-09-252-991A-5987
19	58.8	6.2	1338	4	US-09-270-767-13578
20	58	6.1	420	4	US-09-370-767-15253
21	53.8	5.7	301	3	US-09-222-575-26
22	53.8	5.7	301	4	US-09-389-681-26
23	53.8	5.7	301	4	US-09-620-405B-26
24	53.8	5.7	301	4	US-09-339-338-26
25	53.8	5.7	301	4	US-09-433-826B-26
26	53.8	5.7	301	4	US-09-604-287A-26
27	53.8	5.7	301	4	US-09-285-480-26

28	53.8	5.7	301	4	US-09-834-759-26	Sequence 26, Appl
29	53.8	5.7	301	4	US-09-590-751A-26	Sequence 26, Appl
30	53.8	5.7	301	4	US-09-551-621-26	Sequence 26, Appl
31	51	5.4	1664976	4	US-08-916-421B-1	Sequence 1, Appl
32	51	5.4	1664976	4	US-09-692-570-1	Sequence 180, Appl
33	49.2	5.2	905	4	US-09-663-600A-180	Sequence 154, Appl
34	49.2	5.2	982	4	US-09-663-600A-154	Sequence 60, Appl
35	49.2	5.2	982	4	US-09-621-976-9	Sequence 6989, Ap
36	49.2	5.2	1022	4	US-09-663-600A-60	Sequence 7042, Ap
37	42.4	4.5	1602	4	US-09-252-991A-6989	Sequence 544, App
38	42.4	4.5	2187	4	US-09-221-017B-544	Sequence 106, App
39	41.2	4.3	503	3	US-08-181-271A-106	Sequence 106, App
40	41	4.3	1031	1	US-08-449-315-106	Sequence 106, App
41	41	4.3	1031	1	US-08-444-803-106	Sequence 106, App
42	41	4.3	1031	1	US-08-449-043-106	Sequence 106, App
43	41	4.3	1031	1	US-08-456-265A-106	Sequence 106, App
44	41	4.3	1031	1	US-08-455-416-106	Sequence 106, App
45	41	4.3	1031	1	US-08-455-416-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-09-602-777A-139
Sequence 139, Application US/09602777A
Patent No. 6831165
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oekar
APPLICANT: Habermann, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
FILE REFERENCE: BGI-128CP
CURRENT APPLICATION NUMBER: US/09/602, 777A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932924.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932928.1
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932930.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932933.8
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932935.4
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932973.7
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933002.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933003.4

PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941391.6
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 442
SEQ ID NO 139
LENGTH: 1419
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1396)
OTHER INFORMATION: RXA00152
US-09-602-777A-139

Query Match 18.1%; Score 172; DB 4; Length 1419;
Best Local Similarity 51.7%; Pred. No. 2.2e-41;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

12 CATTATCTTGTGGGAGCGGCTTGGCGCTTCAATCTTGTGTCATCCCA 71
121 CATAGTTTCTGTGCTTGTGCGCGTGTGATCAAGTCATAGCCGATGCCCA 180
72 GCAGAACTCCAGCTGTGAAAGGCTCGGCGTTTCATGCGCCCTGACGGCGTTT 131
181 GGGTGAAGCCCGCATTTGAACGCTTGTAAGTACACCGGCACTGTTGAGGAGCCT 240
132 GAATATTTTGTATTCCTTATGACCGGCGTCCACCGCATTCGCTGAAAGAAATCCC 191
241 GACCTGCTGTGCTTATTCGTGACCGAGTACGCGCAAGATCGACACCCGTGAGCGGT 300
192 TTTAGACGTACCGACGAGTCTGATCAGCGCGATTAATGCAATTAAGTGTGACGG 251
301 GGTCTCATTCACCGCAGCGCTGTTATTAACCAAGACACGACCGTGGCATGATAT 360
252 CATCATCTATTTCAGATCCGATCCAAATCGCTCTCATGCGTTCGACACTACAT 311
361 CGTGTGACCTTCCAAATCAAGCAAGCAGACGCGCATCTAAGGCAATTCATCAT 420
312 TATGCAATTAACCGCTTGGCCAAAGCAGCGTGTCCGTTATCGGCGGTATGCAATT 371
421 CGTGTGTGAGCAGATTTCTGAGCAACTTGAAGCGTGTGCGATGACCT 480
372 GAACAAAGCTTTGAAGACGCGACGAATCAACAGTACCGTCTCGCCCTGATGA 431
481 GGAAGAAACCTCACTTCACTGAGATGATCAACCGCGCTCGTGGCGAGCTGATGC 540
432 AGCCGCGGCGCTTGGGCTGTGAAGTCTTCCTGTTAGAAATCAAGATTTGTTCCGC 491
541 AGCAACCAACCAATGGGCTGTGCGATCAGCGGTGTGAACCTAAGGCAATTCATCC 600
492 GCAAGAAATCTTGGCGCAATGCAAGCAAAATTAACCGCGAAGCGGAAAGCGCCCG 551
601 ACCATCCATCCAGCAATGATGAGAAAGCAGATGAGAGCAGACCGTGAAGCGGCAC 660
552 TATTGCGCAATCCGAGCGCGTAAATGAAACAAATCAACCTTGGCAGTCAAGCTGA 611
661 CATTTTGCAGGAGGCTCAGCGGAAAGCGGACATCAAACTGCGGAAAGGTGAAGCA 720
612 AGCCGAAATTCGAACATCCGAGGAGGCTCAGGCTCGGTCATGCGTCCATGCGGA 671
721 AGCCAAATCTCTCCAAAGCTGAGGAGTGAAGAGCAGCATCATCTCTGAACGAGAGCA 780

672 GAAATGCGCCGCTCAACGCGCGCAAGCGAAATCCCTGCGCTTGTGCGCA 731
781 AGCCAAAGCATGATCTCGCGCGCGGAGGAAAGCGGACGATACCTTCAGGCGCA 840
732 AGCCAAATCCGAGCCATCCGTAATTTGCGCGCG 767
841 GGGTGAAGCCCGAGCAATCCAAAGTCAACGCGAGC 876

RESULT 2
US-08-781-562-2
Sequence 2, Application US/08781562
Patent No. 5763589
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FaelsSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781.562
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
US-08-781-562-2

Query Match 16.4%; Score 155.2; DB 1; Length 1188;
Best Local Similarity 50.5%; Pred. No. 2.3e-36;
Matches 431; Conservative 0; Mismatches 390; Indels 33; Gaps 1;

62 TCATCCCCCAGCAGAGATGCAAGTGTGCAAAAGCTCGGAGCTTTCATGCGCCCTGA 121
182 TCGTCCGCGACAGAGAGCGCTGAGTGTGAGCAATGGCCGATTCACCGATCTCG 241
122 CGGCGGTTTGAATATTGATTCCTTTATCGACCGCGTGCCTACCGCCATTCGCTGA 181
242 AGCTGGTTTGAATCATCTCATCTCTGTGTGAACCGGATCGATATGTGAGAGTCA 301
182 AAGAAATCCCTTTAGAGTACCGACGAGTCTGATCAACCGCGGATTAATGCAATTGA 241
302 AGGAAATTTGATCAAGTGTGAGAGTGTGAGAGTGTGAGATCTGACAAATGTAATCTG 361

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Oy      24 CTGTGACGGCAATCACTATTTCCTCAAGTAAACGATCCCAAACTCGCTCAATACGATTGCA 301
Db      362 AAATCATGATGAGTCTCTTAACTCTCGCATATGGAACCTTTACAAGCAAGCTACGGTGG 421
Oy      302 GCAACTACATTAATGAGCAATTAACCCAGCTTGCACAAAGACGCTGCGTTCCGTTATCGAGC 361
Db      422 AGGACCTGTGATATGCGGTCAACCGAGTACGTCAAAACAACATGATCAAGAGCTCGGCA 481
Oy      362 GTAATGAGTTGGACAAAACGTTTGAAGAACGGACGAAATCAACAGTACCGTGTCTCCG 421
Db      482 AACTCTCTMTGGAACAAAGTCTTCCGGGAAACGGAGATCCCTGATATCCAGCATTTGTGATG 541
Oy      422 CCCCTCATGAAAGCGCGCGGAGGTGTAAGTAAGTCTCTCGTTACGAATTCAGAGATT 481
Db      542 CCATCAACCAAGCTGTGACTGCTGAGGATACCGCTGCTTNCGTATTATAGATCAAGATTA 601
Oy      482 TGGTTCCGCCGCAAGAAATCTTTCCGCGCAATGACAGCAAAATTACCGCCGAAACGCGAAA 541
Db      602 TCCATGTGCCACCCCGGGTGAAGAAAGTATATGCAAGTACAGGTGAGGCAAGCGCGGGA 661
Oy      542 AACGCGCCGCTATTGCCGAATCCGAAGGCCGTTAAAATGCAACAATCAACTTGCAGATG 601
Db      662 AACGGGCCACAGTTCTAGAGTCTGA-----GG 688
Oy      602 GTACAGCTGAAAGCCGAAATTCACACATCCGGAAGCGAGGCTCAGGCTCGGTCATGCGT 661
Db      689 GGAACCCGAGGTGGCGCATTAATGTGGCAAGAAAGGAAAGAAACGGCCCAAGATCTGGGCT 748
Oy      662 CCAATGCGGAAGAAATGCGCCGCATCAACCGCGCCAAAGCGGACGGAATCCCTGCGCC 721
Db      749 CCGAAGCAAGAAAAGCGCTGAACAGATTAATACGACAGCAGAGAGAGGCCAGTGCAATGTTCCG 808
Oy      722 TTGTTGCCGAAGCCAAATGCCGAAGCCATCCGTCAATTGCGCGCCCTTCAAAACCAAG 781
Db      809 CGAAGGCCAAGGCTAAAGCTGAAGATTCGATTCGATCCTGGCTCAGACTCTGACACAACATA 868
Oy      782 GCGGGGCGGATGCGGCTCAATCTGAAGATTGCGGAACAATGCTACCGCGGTTCAAACATC 841
Db      869 ATGAGATGTGAGGAGCTTCACTGACTGATGAGCGGAGAGATGTACAGCGGTTCTCCAAAC 922
Oy      842 TTGCGCAAGAAAGCAATACGCTGATTATGACCGCCCAATGTTSCGCAATTCGACAGCCTGA 901
Db      929 TGCGCAAGAGACTCAACACATATCTTACTGCTCTCCAAACCTTGGCAATGTCAACAGATGG 988
Oy      902 TTTCTGCGCGCATG 915
Db      989 TGGCTCAGAGCATG 1002

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OR INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g

```

```

US-09-103-840A-2
Query Match 16.2%; Score 153.2; DB 3; Length 4403765;
Best Local Similarity 50.0%; Pred. No. 3,9e-34;
Matches 383; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

QY 2 TGAATTTTCATTATCTGTGTGTCAGACCCGTGCGCTTTTCGAGCTTCAAAATCTTGTGCG 61
DB 1677551 TGGTGTTTCTGCGCGCTCTGTGTATTTTGGCATTATCGTGTGTGGCCAACTGCGTGGCGC 1677610
QY 62 TCATCCCCCAGCAGAAAGTCCACGTGTGCAGAAAGGCTCGGGCGTTTCATCGCGCCTGA 121
DB 1677611 TGAATCCGCGAGCGCGAGCCGCGGTGATCCAGCGCGCTGCGTATAGTCGTGACGTCA 1677670
QY 122 CGCGCGGTTTGAATTTTATTTATTTCCCTTTATCGACCGCGCGCTACCCGCAATTCGCTGA 181
DB 1677671 GTGGGCAAGTGAACGCTTGTGTGTGCGCTTATTCACACGCGTCCGGGCTCGGTGTGACTGC 1677730
QY 182 AAGAAATCCCTTTTGAAGTGAACCCAGCCAGCTGTGCATTCACGCGCGATTAATACCAATGA 241
DB 1677731 GCGAGCGGCTGTGTGTCTGTTTCCGCGCGAACCGGTGATTCACGAGAACAACTTACGCTGA 1677790
QY 242 CTGTTGACGGCATCATTTATTTTCCAGTAACCGATCCCAACTCGCCTCATACGTTTCCA 301
DB 1677791 ACATCGACACCGTGTCTTACTTCCAGGTGACCGTTCCGACAGCGCGCGGTGTACGAGTCA 1677850
QY 302 GCAACTCATTTATGCGCAATTAACCAAGTTGCGCCAAAGCAAGCGCTGCTTCCGTTATGCGGC 361
DB 1677851 GCAATTTACATGCTGTGGGGTGCAGAACGTCTCACACACACACCTCTGCGAGAGTTGCGCG 1677910
QY 362 GTATGAGATTGGAACAAACGTTTGAAGAAAGCGACGAAATCAACAGTACCGTGTCTCCG 421
DB 1677911 GGAATGACGTGTGACACAGCTTTGACTCTGCGGTGACACAGATTCACGCCACTGCGCGCG 1677970
QY 422 CCTCGATGTAAGCGCGCGGGGCTTGGGGTGTGAAGTCTCCGTTACGAAATCAAGATT 481
DB 1677971 TTCTGATGAGGCGACCGCGCGCTGTGGGGTCTGCGGGTGTGCGGGGTGAGACTGCGCAGCA 1678030
QY 482 TGTGTTCCGCGCGCAAGAAATCTTTCGCGCATTCGACGCGACAAATTAACCGCCGACGCGAAA 541
DB 1678031 TCGATTCGCGCGCTCTCGATTTCAGGCGTGTGATGGAAGACAGATGAAGCGCTGACCGGAGA 1678090
QY 542 AAGCGGCGCGTATTTGCGGAATCCGAGAGCGGTAAATTCAGAAATCAATCAACTTGCACGTG 601
DB 1678091 AGCAGGCGATGATTTCTGACCGCGCGAAGATACCCGGAGGCGCGGATTAACACAGCGCAGG 1678150
QY 602 GTCAAGCTGTAAGCCGAATCCACATTCGAGGCGAGGCTCAAGGCTGCGGTCAATGCGT 661
DB 1678151 GGCAGGAGCGAGCGCGAATCTGTGCGCGCGCGAGGCGCGCAAGCAGCGCGCATCTTGTCTG 1678210
QY 662 CCAATGCCGAGAAATGCGCGCGCATCAACGCGCGCAAGCGCAAGCGGAATCCTTGGCGCC 721
DB 1678211 CTGAGGCGGATCGCGAGTCTGTGATGTGTGGCGCTCAAGGCTGAGCGCGCGCGCTTACC 1678270
QY 722 TTGTTCCGAAGCAATGCGGAGCCGATCCGTCGAATTTGCGCGCGC 767
DB 1678271 TGCAGGCGCAAGGCGAGGCGCAAGGCGCATTCAGAGAAAGACTTGC CGC 1678316

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 2436-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 441529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 16.2%; Score 153.2; DB 3; Length 441529;
Best Local Similarity 50.0%; Pred. No. 3.9e-34;
Matches 383; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

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Oy 2 TGAATTTTCAATATCTTTGGAGCCGTCGCGTTTGCGCTTCAATCTTTGCG 61
Db 1677417 TGGGTTTCTGCGCCGCTCTGATGATTTTCGCCATCATCTGTGTGCCAAGTCGGTGGCGC 1677476
Oy 62 TCATCCCCAGAGAGAGTCCACGTTGTGAAAGGCTCGGCGTTTCCATGCGCCCTGA 121
Db 1677477 TGATCCCCAGAGAGGCGCGGATGATGAGCGGCTGGCTATAGTGTGTAAGGTCA 1677536
Oy 122 CGGCGCGTTTGAATATTTTGAATCCCTTATCGACCGGTGGCGCTACCGCATTCGCTGA 181
Db 1677537 GTGGCAGTTGACCGCTGTGTGGTCCGTTCAATGACCGGCTCGGCTGGAAGCTGC 1677596
Oy 182 AAGAAATCCTTTAGACGTACCCAGCCAGCTCTGATCAGCGCGATTAATACGAATTGA 241
Db 1677597 GCGAGCGGTGTGTGCTTTCGCGCAACCGGTGATCAACGAGAGCAACTGAAGCTGA 1677656
Oy 242 CTGTGACGGCATCTATTTCAGATGTAACCGATCCCAACTCGCTCATACGGTTGCA 301
Db 1677657 ACATGACACCGGTGTACTTCCAGGTGACCGTTCCCAAGCGCGGTGTACAGATCA 1677716
Oy 302 GCAACTATATATAGCAATTAACCAAGCTTGCCCAACGACGCTGTTCCTTAACTCGGCG 361
Db 1677717 GCAATTAATGTCGGGTGCAACGCTCACCAACCACTGTGCAACGTTGTGCGCG 1677776
Oy 362 GTATGAGTTGAGCAAAAGTTTGAAGACGCAAGCAATCAAGTACCGTCTGCTCG 421
Db 1677777 GGAATGACGTGAGAGACGTTGACCTGCGGTGACCAATCAACCGCAAGCTGCGCGCG 1677836
Oy 422 CCTTCGATGAACCGCGCGGCTTGGGGTGTGAAGTCTCTCGTTACGAATCAAGATT 481
Db 1677837 TTCTCGATGAGCGCACCGCGCTGGGGTGTGGCGGTGAGCTGCGCAGCA 1677896
Oy 482 TGTGTTCCGCGCAGAAATCTCTCGCGAATGCAAGCAAAATTAACCGCCGAGCGGAA 541
Db 1677897 TCGATCCGCGCGCTGATTCAGGCGTGAAGAAAGCAATGAAGGCCAGCGGAGGA 1677956
Oy 542 AACGCGCCGTATTGCGCAATCCGAATCCGTAATAATCAAAATCAACTTGCAGATG 601
Db 1677957 AGCGAGCATGATTTCTGACCGCCGAAGGTACCGGAGGCGCGCATTAAGAGCGCGAGG 1678016
Oy 602 GTCAAGCGTGAAGCCGAATCCGAATCCGAAGCGGAGGCTCAGGCTCGGCTCAATGCGT 661
Db 1678017 GGCAGAAAGCAGCGCAGATCTTGGCGCGCGAGGCGCAAGCGCCGATCTTGCTG 1678076
Oy 662 CCAATGCCGAGAAATCCGCGCATCAACCGCGCCAAAGGGAAGCGGAATCCCTGCGCC 721
Db 1678077 CTGAGCGCGATCGGAGTCTCGGATGCTGCGCGCTCAGAGGTGAAGCGCGCGGCTTAC 1678136
Oy 722 TTGTTGCCGAGACCAATGCGGAGCATCCGTCAAATTTGCCGCGCG 767
Db 1678137 TGCAGCGCAGAGGCGAGGCCATGAGAGACCTTGCGCGCG 1678182
```

RESULT 5
US-09-543-681A-2806
; Sequence 2806, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2806
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2806

Query Match 14.9%; Score 141.4; DB 4; Length 963;
Best Local Similarity 52.7%; Pred. No. 2.9e-32;
Matches 307; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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Oy 87 TGTGAAAGGCTCGGGGTTTCCATCGCGCCCTGACGCGCGTTGAAATTTGATTC 146
Db 129 TGTGAGCGTTTGGAGTTATACAGTACCGTTCAGGCGCTTCACTCTTATTC 188
Oy 147 CTTATGACCGCGCTCGCCTACGCGCATTCGTAAGAAATCCCTTAGACGTAACCG 206
Db 189 ATTATTTGACCGTATTTGCTGCTGATTAATATGATGAAACATATTCCTTC 248
Oy 207 CCAAGCTGATCAACGCGCGATTAATACGAATTGACTGTTAGCGCATCTATTTCA 266
Db 249 TCAAGAGTGAATTTCTGATTAATGCAATGTCAGATTAATGCGGCTGCTTATTTCA 308
Oy 267 AGTAACGATTCCAACTCGGCTCATACGTTGCAAGCACTCACTATTAATGCAATACCA 326
Db 309 AGTATGATTCAGTAAAGCTGTATGAGTAAATTAACCTAGCTTGCATATCAATCA 368
Oy 327 GCTTCCCAAAAGCAAGCGCGGCTTCCGTTATCGGCGGTATGAGTGAAGTGAAGT 386
Db 369 TCTAACGTTACCAATATCCGTAATGCTTATGAGCTCTATGAACTGATGAATTTCTTC 428
Oy 387 AGAAGCGACGAATCAACAGTACCGTCTCCGCTCGATGAGCGCGCGGCTTG 446
Db 429 ACAAGGTATGATCAATGACCGTTATTAATGATGATGATGATGATGATGATGATGATG 488
Oy 447 GGGTGTGAAGTCTCGGTTACGAATCAAGATTTGTTCCGCGCAAGAAATCTTTC 506
Db 489 GGGTATTAATTAATCCGTTATGAAATTCGATGATGCGCCCAACAGCTTAATTTTC 548
Oy 507 CGCATGAGGCAAAATTAACCGCGAAGCGGAAAGCGCGGCTATGCGGATCCGA 566
Db 549 TGCATGATGCGCAATGAAGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 608
Oy 567 AGCGCTAAATTCGAATCAACTTGCAGTGTGACGCTGAGGTAAGCGGAATTCACA 626
Db 609 AGGATCCGTAACGCGGAATCTTAAGGGAAGGTAAGGGAAGGGAATCTTAAA 668
Oy 627 ATCCGAAGCGAGCTGAGGCTGCGGTCATGCGTCCATGCC 669
Db 669 AGCAGAGGTGAACGTGATGCTTCTTAAGCGGAAGCC 711
```

RESULT 6
US-09-489-039A-6125
; Sequence 6125, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6125

LENGTH: 951
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
us-09-489-039a-6125

Query Match 13.7% Score 130.2; DB 4; Length 951;
Best Local Similarity 51.9%; Pred. No. 6,8e-29;
Matches 294; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

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QY 88 GTGGAAGGCTGGGCGTTTCATCGCGCCCTGACGCGCGGTTTGAATTTGATTC 147
DB 124 GTGAGCGCTTGGGCGTTTACCAAGACGTGACGCGGAGTTAAGTTAGTCGCG 183
QY 148 TTTATGACCGCGCTTACCGCCATTGCTGGAAGAAATCCCTTTAGACGTAC 207
DB 184 TTTATGACCGGTATCGCGCGCAAGTGAAATATGAGACAGGTGCTCATTCCT 243
QY 208 CAGGTCTGATCAGCGGATATATGCAATTTGATGAGGCGATCATTTATTC 267
DB 244 CAGGAGTTATCTCCGGATTAACGCAAGTCATGACGCGGTCTGCTTTATTC 303
QY 268 GTTACCGATCCCAATCTCGCTCATACGGTTCGAGCACTATATGCAATTA 327
DB 304 GTGATGACGCGCCCAAGGCGCCCTTACGAGTCAGCAATCTTGAAGCGAT 363
QY 328 CTTCGCCAAGCAGCGCTGCTTCCGTTATCGGCGCTATGAGATTGACAA 387
DB 364 CTGAGATGACCAACATCCGTACCGGTCTCGCTCATGAGCTGAGCAAT 423
QY 388 GAAACCGAAGAAATCAAGTACCGTCTCGCGCTGATGAAGCGCGGCGCT 447
DB 424 CAGCGGACAGATTAAACCGCGCTGCTGATGTTGACGACCAACCAAC 483
QY 448 GGTGTAAGTCTCTCGCTTACGAAATCAAGATTTGTTCCGCGCAAGAA 507
DB 484 GGGGTGAATATCAACCGCGCTCGAAATTCGCGAGCTTCGCGCGAGCT 543
QY 508 GCAATGACAGCAAAATTAACCGCGCAAGCGGCGCGCTTATTCGCA 567
DB 544 TCGATGAAGCGCCAGATGAAGCGCAACGCGCGCTGATCATCTTGA 603
QY 568 GGCCTGAATATGAACAAATCAACCTTGCAGTGTCAAGCGGAAATCA 627
DB 604 GGGGTGCGCAGCGCGAAATTTCTGAAGCGGAAAGCAATGCGAGTCT 663
QY 628 TCCGAAGCGGCTCAGCGCTGCGGTC 654
DB 664 GCGGAGGCGAAGCGGATCGCGGTC 690
```

RESULT 7
US-09-902-540-4035
Sequence 4035 Application US/0902540

Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4035
LENGTH: 1107
TYPE: DNA
ORGANISM: Myxococcus xanthus
us-09-902-540-4035

Query Match 11.9%; Score 113; DB 4; Length 1107;

Best Local Similarity 51.1%; Pred. No. 1.1e-23;
Matches 266; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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QY 216 CATCAGCGCGATTAATACGAATTAAGTGTGAGCGGATCATCTTTCCAGTAAC 275
DB 264 CATCAGCGCGATTAATACGAATTAAGTGTGAGCGGATCATCTTTCCAGTAAC 323
QY 276 TCCCAACTCGGCTCATCGGTTTCAGGCACTATATGCAATTAACAGCTTGCCA 335
DB 324 GCGCGGAAAGGCGCTTACAGGTGAAGAACTCGCGCTCGCATGAGAGCTCAGAT 383
QY 336 AACGACGCTGCTTCCGTTATCGGCGATGAGATTGACAAACGTTGAAGACGCG 395
DB 384 GACGAACTGCGCAACATCATGAGCGGCTGACGTGACCAAGCGCTCACAGCGCG 443
QY 386 GCAATTCACAGTACCGTCTCGCGCTGATGAACCGCGGCGCTTGGGGTGTGA 455
DB 444 GACGCTCAACCAAGCTGCGCATGTCTGACAGGCAACCGAAGTGGGGCTCA 503
QY 456 AGTCTCGTTACGAATCAAGATTGTTGTTCCGCGCAAGAAATCTTCGCGCATGCA 515
DB 504 GGTGACGCGCTGAGCTGCGCAATGAGCGCTCCAGGCTCATAGGCGCGCATGCG 563
QY 516 GGCACAAATTAACCGCGCAACGCAAAACGCGCCGTTATGCGAATCGAAGCGTAA 575
DB 564 CAGGAGATGACCGCGGAGCTGAGCGCGCGCGAGGTCAACAGCGCGAGGCGACAA 623
QY 576 AATGCAACAAATCACTTGCAGTGTGACGTGAAGCGCAATTCGAATTCGGAAG 635
DB 624 GCGCGCGCATCTTCAGGCGGAGGCGAAGAAATCTCCCATCTTCGCGCGAGGCG 683
QY 636 CAGGCTCAGGCTGCGGTCAATGCGTCCAAATGCGAAGAAATGCGCGCATCAACGCG 695
DB 684 CCAACGCGACGCGGAGATTGCGCGCGCAAGGCAACAGCGCGCATCTGCGAGCG 743
QY 696 CAAAGCGAAGCGAATCCCTGCGCTTGTTCGCAAGCA 736
DB 744 GGAAGCGAAGCGGAGCGGACCGCGGCTGCTTGAAGGCA 784
```

RESULT 8
US-09-902-540-1200
Sequence 1200 Application US/0902540

Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1200
LENGTH: 24986
TYPE: DNA
ORGANISM: Myxococcus xanthus
us-09-902-540-1200

Query Match 11.9%; Score 113; DB 4; Length 24986;
Best Local Similarity 51.1%; Pred. No. 4.5e-23;
Matches 266; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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QY 216 CATCAGCGCGATTAATACGAATTAAGTGTGAGCGGATCATCTTTCCAGTAAC 275
DB 9409 CATCAGCGCGATTAATACGAATTAAGTGTGAGCGGATCATCTTTCCAGTAAC 9468
QY 276 TCCCAACTCGGCTCATCGGTTTCAGGCACTATATGCAATTAACAGCTTGCCA 335
DB 9469 GCGCGGAAAGGCGCTTACAGGTGAAGAACTCGCGCTCGCATGAGAGCTCAGAT 9528
```


QY 336 AACGACGCTGCGCTTCGTTATCGGCGGATGAGTTGACAAACGTTTGAAGAACGGA 395
| | | | |
DB 9529 GACGAACTGGGCAACATCATATGCGGGGGGTGACGCTGAGCAGACGCTCACACGCGGGA 9588
| | | | |
QY 336 GGAATTCACAGTACCGCTGCTTCGCGCTTCATGAGACCGCGGGGCTTGGGGTGTGA 455
| | | | |
DB 9589 GACGCTCAACACCAAGCTGCGCATGCTGAGACAGGCGCACCGAAGTGGGGGCTGA 9648
| | | | |
QY 456 AGTCTCGCTTACGAATTCAGATTTGGTTTCGCGGGAAGAAATCTTCGGGCAATGA 515
| | | | |
DB 9649 GGTGACGCGCGTGGAGCTGCGGAAATCAGCTCGCCGACATCAAGCGCCGATGAC 9708
| | | | |
QY 516 GGCACAAATTCACCGCGGACGCAAAACGCGCCGATTTGCGGATTCGGAAGCGCTGA 575
| | | | |
DB 9709 CAGAGATGACCGCGGAGCGGTGAGCGCGCGCCAGGTCACCAAGCGCGAGGCGACGA 9768
| | | | |
QY 576 AATGCAACAAATCACTTGGCAGTGTGACGCTGAAGCGGAATTCACCAATCCGAAG 635
| | | | |
DB 9769 GCGCCGCGCATCTTCAGGCGCGAGGCGGAGAAATCTCCGCTTCGCGCGGAGGC 9828
| | | | |
QY 636 CGAGGCTCAGCTGGCTCAATGCGTCCAAATCGGCAAAATCGCCCGATCAACCGGC 695
| | | | |
DB 9829 CGAACCGACGCGAGATTGCGCGCGCGGAGGCGACAGCGCGCACCATGCTGACAGC 9888
| | | | |
QY 696 CAAAGCGGAGCGGATCCCTGCGCTTGTGTCGGAAGCCA 736
| | | | |
DB 9889 GGAAGCGAAGCGCGGACCGGCTGCTTCGAGGCA 9929
| | | | |

RESULT 9
US-09-902-540-6837
; Sequence 6837, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6837
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6837

Query Match 11.0%; Score 104.2; DB 4; Length 840;
Best Local Similarity 51.7%; Pred. No. 4.2e-21;
Matches 263; Conservative 0; Mismatches 243; Indels 3; Gaps 1;
QY 62 TCATCCCCAGAGAAATGTCAGTTCGAAAGGCTGGGGCTTTCATCGCGCCCTGA 121
| | | | |
DB 77 TCGTCAAGAGTACCAAGACGCGGTGTGTTCCGCTGGGCGCTTCGCGGCTCAAC 136
| | | | |
QY 122 CGGCGGTTTGAATATTTTGAATTCCTTATGACCGCGTCCATCCGCCATTCGCTGA 181
| | | | |
DB 137 GCGGCGGCTTCGCTGAGCTATCCCTTCGTGAGCGATGTATCATTCAGCTGCGCA 196
| | | | |
QY 182 AAGAAATCCCTTAAAGTACCAAGCGAGTGTGATCAAGCGGCAATATACGCAATTGA 241
| | | | |
DB 197 TCG---TGGCCGAGCGGCTTCACAGAGATGATACCCGGGACCAAGTCAAGCTGA 253
| | | | |
QY 242 CTGTTGACGAGCATCATTTTCAAGTAAACGATCCAAATCCGCTCATACGCTTGA 301
| | | | |
DB 254 AGGTAAAGCGGCTGTCTTACCTTCGCGCTCATCAAGCGGACCAAGCGCTGCTCAAGGTG 313
| | | | |
QY 302 GCAACTACATTAATGCAATTAACCAAGCTTCCCAAGCAAGCGCTGCTTCGTTATCGGCG 361
| | | | |

DB 314 AGGACTACCTTATGCCACAGCCAGCTCGGCCAGACGACCTCGCTCCATCTCGGCGC 373
| | | | |
QY 362 GTATGAGTTGAGCAAAACGTTTGAAGACCGCAAGAAATCAAGTACGCTGCTCCG 421
| | | | |
DB 374 AGTGAAGTGAACCAAGCTCTCTTCAGCGGGAGCGCATACCAAGATTTACGACAG 433
| | | | |
QY 422 CCTTCGTAAGACCGCGCGGCTTGGGGTGTGAAGTCTTCCTCGTTACGAATCAAGATT 481
| | | | |
DB 434 TGTCTGATGACGCAACGACCGGTGGGGCGTCAAGGTGTCCAAAGTGAAGTGAAGCA 493
| | | | |
QY 482 TGTTCGCGCGCAAGAAATCTTGGCGGATGACAGGCAAAATTAACGCCGAAGCGGAA 541
| | | | |
DB 494 TCGACCTGCGCGGAGATGACGCGGCTATCGCGCGGACGCGGCGAGCTGAGCGCAGC 553
| | | | |
QY 542 AACGCGCCGATTTGCCGAATCCGAAGGC 570
| | | | |
DB 554 GCGGCGCAAAATCATGCTCGCGCGAGGCG 582
| | | | |

RESULT 10
US-09-902-540-571/C
; Sequence 571, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 571
; LENGTH: 4026
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-571

Query Match 11.0%; Score 104.2; DB 4; Length 4026;
Best Local Similarity 51.7%; Pred. No. 8.7e-21;
Matches 263; Conservative 0; Mismatches 243; Indels 3; Gaps 1;
QY 62 TCATCCCCAGAGAAATGTCAGTTCGAAAGGCTGGGGCTTTCATCGCGCCCTGA 121
| | | | |
DB 3292 TCGTCAAGAGTACCAAGACGCGGTGTGTTCCGCTCGGCGCTTCGTGGGCTCAAC 3233
| | | | |
QY 122 CGGCGGTTTGAATATTTTGAATTCCTTATGACCGCGTCCATCCGCCATTCGCTGA 181
| | | | |
DB 3232 GCGGCGGCTTCGCTGAGCTATCCCTTCGTGAGCGATGTATCATTCAGCTGCGCA 3173
| | | | |
QY 182 AAGAAATCCCTTAAAGTACCAAGCGAGTGTGATCAAGCGGCAATATACGCAATTGA 241
| | | | |
DB 3172 TCG---TGGCCGAGGAGTGTCTTCACAGAGATGATACCCGGGACCAAGTCAAGCTGA 3116
| | | | |
QY 242 CTGTTGACGAGTATCATTTTCAAGTAAACGATTCGCAACTCGGCTCATACGCTTGA 301
| | | | |
DB 3115 AGGTCAAGCGGTGTCTTACCTTCGCTCATTCACCGGCAAGAGCGGTGCTCAAGTGG 3056
| | | | |
QY 302 GCAACTACATTAATGCAATTAACCAAGCTTGGCCCAAGCAGCGCTGCTTCGTTACGGGC 361
| | | | |
DB 3055 AGGATACCTTATGACCAAGCGAGGCTGCGCTCAGAGAGAGCTGCTCATCTCGGCGC 2996
| | | | |
QY 362 GTATGAGTTGAGCAAAACGTTTGAAGACGCAAGAAATCAAGTACGCTGCTTCG 421
| | | | |
DB 2995 AGGTGAAGCTGACAGAGCTCTTCAGAGCGGAGCCATCAACACAGAGATTGACAGG 2936
| | | | |
QY 422 CCTTCGTAAGACCGCGCGGCTTGGGGTGTGAAGTCTTCGTTACGAATTCAGAGATT 481
| | | | |
DB 2935 TGTCTGATGACGCAACGACCGGTGGGGCGTCAAGGTGTCCAAAGTGAAGTGAAGCA 2876
| | | | |

QY 482 TCGTCCCGCCGAGAAATCTTCCGCAATGACGACAAATACCCGCCAAGCGGAA 541
| | | | |
DB 2875 TCGACCTGCGCCGAGATGACGCGGCATCGCGGAGCGGAGCGCTGAGCGGAGC 2816
| | | | |
QY 542 AACGCGCCGCTATTGCGCAATCCGAAGGC 570
| | | | |
DB 2815 GCCGCGCCGAAATCATCGCCGCGGAGGCG 2787
| | | | |

RESULT 11
US-09-328-352-126
; Sequence 126, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 126
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-126

Query Match 10.1%; Score 96; DB 4; Length 870;
Best Local Similarity 46.4%; Pred. No. 1.3e-18;
Matches 312; Conservative 0; Mismatches 360; Indels 0; Gaps 0;

QY 8 TTTTCATATCTTGTGGAGCGCGTGGCGTTTGGCTTCAATCTTTGTGTCATCC 67
| | | | |
DB 35 TTGTTTACCTTTTGGCTTTGTGTGCTGTACATTTTAAAGGGTACGTAATGTTC 94
| | | | |
QY 68 CCCAGAGAGATGCCAGTGTGCGAAGGCTCGGCGTTTCCATCGCGCCCTGACGCGG 127
| | | | |
DB 95 CTCAGAGCTATTAATGATTTGTACAGCTTAAAGAAATATCTTACGCTTAATCTG 154
| | | | |
QY 128 GTTTGAATATTTTATTCCTTATGACGCGGCTGCTACCGCATTCGCTGAAGAA 187
| | | | |
DB 155 GCTTAACTTCTGTTATCTTATTTATGATGATGTAGCTTAAAGTACACATTAAGATA 214
| | | | |
QY 188 TCCCTTTAGACGTAACCCAGCGAGTGTGATCAGCGCGCATTAATGCAATGACTGTG 247
| | | | |
DB 215 TTGTGCTGATATTCATCAAGAGATGATTAACCGGTGCAATGCTGATTAATCATGA 274
| | | | |
QY 248 AGGCGATCATTTATTTCCAAAGTACCGATCCAACTCGCTCATACGTTGCAAGCACT 307
| | | | |
DB 275 ATGCCCTGCGTATATCAATCTGACTACCTGAAAAAGCGGTGTACGGTATTGAAAATC 334
| | | | |
QY 308 ACATTAATGCAATTTACCGAGCTTGGCCAAACGACGCGGCTTCCGTTATCGGCGATAG 367
| | | | |
DB 335 ATACATGCGCATTCGAACCTTTGACGATCTTACCTTCAATTTGCGGTAATG 394
| | | | |
QY 368 AGTTGACAAACGTTTGAAGACGCGAGAAATCAACATCCGTCCTCCGCCCTCG 427
| | | | |
DB 395 ATCTAGATGATGCCATATCTTCAACGAGTACATTAAGCTAACTAAAGCTGCAATTT 454
| | | | |
QY 428 ATGAAGCCCGCGGCGCTTGGGCTGTGAAGTCTCCGTTACGAATCAAGATTTGTTTC 487
| | | | |
DB 455 CTGATGATATTTCAAGTTGGGCTATCATTTTAAAAACAGTAGAAATTTCAAGATTTCAAG 514
| | | | |
QY 488 CCGCGCAAGAAATCTTCCGCAATGACGACAAATTAACCGCGCAAGCGGAAACGCG 547
| | | | |
DB 515 CATTTCAACCATGCAAGCTGCGCATGAACTCAAGCGCTGCTGAACGTCACGTCGTG 574
| | | | |
QY 548 CCGATTTGCGCAATCCGAAGCGCGTAAATCGAACAAATCAACTTTCGCGATGTCAGC 607
| | | | |
DB 575 CTACATTTACAAAGCTGATGTGAGAAACAAGCTCAATTTTGAAGAGATGTCGTT 634
| | | | |
QY 608 GTGAAGCCGAAATCAACATCCGAAGCGAGCTCAGGCTGCGGTCAATGCTCAATG 667
| | | | |

DB 635 TAGAAGCATCTCGCGGTATGCGGAAGCTCAGGTTGTTTACGACAAAGCTTCAAAAAG 694
| | | | |
QY 668 CCGAAGAAATCG 679
| | | | |
DB 695 CGATTGAATAG 706
| | | | |

RESULT 12
US-09-540-236-1751
; Sequence 1751, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1751
; LENGTH: 885
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-1751

Query Match 8.9%; Score 84.6; DB 4; Length 885;
Best Local Similarity 47.9%; Pred. No. 3.4e-15;
Matches 243; Conservative 0; Mismatches 264; Indels 0; Gaps 0;

QY 109 CATCGCGCCCTGACGCGCGGTTTGAATATTTGATTCCTTTATGACCGCGCTGCTAC 168
| | | | |
DB 145 CACCAACACCTGAGCGCGGCTGAAATTTTATTTATTTCTATGATGATCTGCTGAT 204
| | | | |
QY 169 CCGCATTCGCTGAAGAAATCCCTTTAGACGTAACGACGAGTGTGATCAAGCGCAT 228
| | | | |
DB 205 AAGTAACACCAAGAAATGATCTGATCTGATATCCAAAGCAAGATCAATACGCTGAT 264
| | | | |
QY 229 AATAGCAATGATCTGTTGACGCGATCATCTATTTTCAAGTAACGATCCCAATCGCC 288
| | | | |
DB 265 AATGCTGATCATGCGCAATGAGTGCATATTAATTTGTCAGCTGACATGCA 324
| | | | |
QY 289 TCATACGTTGACGAACTACATTAATGCAATTAACCGCTTGGCCAAACGAGCTGCGT 348
| | | | |
DB 325 GTCTATGCGATGAATATTAACATGCGATTCGTAATTTGATCAACATCTTAACG 384
| | | | |
QY 349 TCCGTTATCGCGCGTATGAGTGTGACAAACGTTTGAAGAACGCGACGAAATCAACAT 408
| | | | |
DB 385 TCTATCATGCGTGAATGATGATTTGATGCGGCTTATCAAGTGTGACCAAAATTAAGCA 444
| | | | |
QY 409 ACCGTGCTCGCGCTGATGAAGCGCGGCGCTTGGGCTGTGAAGTCTCCGTTAC 468
| | | | |
DB 445 CAGCTTAAACAGCATCAGTATGATGATCAATTTGATGTTGGGAAATTAACCTTAACCTGTG 504
| | | | |
QY 469 GAATCAAGATTTGTTTCCGCGCAAGAAATCTTCCGCAATGACGACCAATTAAC 528
| | | | |
DB 505 GAATTCGAAGATCAAGCATGACGACCAATGCAATTTGCGATGAGAAACAAGCGCT 564
| | | | |
QY 529 GCGGAAGCGGAAGAAACGCGCGCTATTTGCGGATCGAAGCGCTTAAATCGAACAAATC 588
| | | | |
DB 565 GCTGAGCTTCAACGCGCTGTCACCGTCAACCGTGCAGATGTCAAAAACAAGCGGCATC 624
| | | | |
QY 589 AACCTTGCAGTGTGTCAGGCTGAAGCC 615
| | | | |
DB 625 TTGAAGCAGATGCGCGCTGAAGAGCC 651
| | | | |

RESULT 13
US-09-596-002-39
; Sequence 39, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.

APPLICANT: Paterson, Chandra
APPLICANT: Beig, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 39
LENGTH: 100848
TYPE: DNA
ORGANISM: M. catarrhalis
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte template ID No. 6632636 39
PUBLICATION INFORMATION:
US-09-596-002-39

Query Match 8.9%; Score 84.6; DB 4; Length 100848;
Best Local Similarity 47.9%; Pred. No. 3e-14; Mismatches 264; Indels 0; Gaps 0;
Matches 243; Conservative 0;

QY 109 CATCGCGCCCTGACGCGCGTTTGAATATTTTGAATTCCTTTATGACCGCGCTCCCTAC 168
DB 15208 CACCAACACTTGACCGCGGTGTAATTTTATTTCTTAATGAGATGCTGCGCTAT 15267
QY 169 CGCCATGCTGAGAAATCCCTTTAGACGACCGAGGTCTGCATCAGCGCGCAT 228
DB 15268 AAGTACCAACCAAGACATCTTACTGATATCCCAAGCAAGAGTCAATTAACGCGTAT 15327
QY 229 AATACGCAATGACGTGACGCGCATCATTTTCCAGTAAACGATCCCAACTCGCC 288
DB 15328 AATGTCATATGATCCCAATGCGCATATTAATTTGTCAGCTGAGCATGCA 15387
QY 289 TCATACGCTGACGACATCAATTATGCAATTAACCAAGCTTCCCAACGACGCTGCT 348
DB 15388 GTCATGCGATGAAATTTATGACATGCGCATTCGTAATTTGTAACAAATCCTTAAGC 15447
QY 349 TCCGTTATCGGCGGATGAGTTGACAAACGTTTGAAGAACGCGAGCAATCAACGT 408
DB 15448 TCTATCATCGGAGATGATTTGATGCGCGCTTATCCAGTCGACCAATTAACCA 15507
QY 409 ACCGTCGTCGCGCTCGATGAGCGCGCGGCGTGGGAGTGAAGTCTCCGTTAC 468
DB 15508 CAGCTAAAACGCGCATGATGATCAATTTCTGATTTGGGAAATTAACCTAAACTGTG 15567
QY 469 GAATCAAGATTTGTTCCGCGCAAGAAATCTTCGCGCAATGCAAGCACAATTAAC 528
DB 15568 GAATCAAGATCAAGCATCAAGCATCAAGCAATGCGATGAGAGCAAGCGGC 15627
QY 529 GCCGAACGCAAAACGCGCGCTTATTTGCGCAATCCGAAGCGCGTAATGCAACAATC 588
DB 15628 GCTGCGCTCAACGCGCTGCGCAACCGCTGCGATGTCGCAAAACCAACCGCGCATC 15687
QY 589 AACCTGCGAGTGTGACGAGTGAAGCC 615
DB 15688 TTAGAAGCATGCGCGCTTAAGAGCC 15714

RESULT 14
US-09-252-991A-5885
Sequence 5885, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5885
LENGTH: 558
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5885

Query Match 8.1%; Score 77; DB 4; Length 558;
Best Local Similarity 49.7%; Pred. No. 5.3e-13; Mismatches 251; Conservative 0; Indels 4; Gaps 2;

QY 9 TTTCATTAATCTTTGTCAGCGCGTTCGCGTTTTCGCGTCAATCTTTGTCATCC 68
DB 30 TTGGCAATGTTGCTGATGTTCTTCGCGCTGCTGTCATGCGCGCTGCGCATCTCCG 89
QY 69 CCAGAGAGAGTCCACGTTGTCGAAAGCTCGGCGTTTCCATGCGCGCTGACGCGCG 128
DB 90 CGAGTACGAGCGCGCGCTGTCGATTCAGCTCGCGGCTTTCGAAAGTCAAGGCGCGCG 149
QY 129 TTGGAATTTTGAATTCCTTTATGACCGCGTGCCTTACCGCATTCGTCGAAAGAAAT 188
DB 150 GCTGTCGTCGATTCCTCGGATTCAGCAAGATG--TGCGATTCGACCTGCGCACCAT 206
QY 189 CCTTTAGACGTACCCAGCGAGTCTGCATCAGCGCGCATTAATAGCAATTAATCTTTGA 248
DB 207 GCTCTGACGCTGCGCGCGAGATGATTTTCCGCGACAAGTTTCGTCGTAAGTCAA 266
QY 249 CGGATCATCTTAATTTCCAGTACCGATCCCAACTCGGCTCATTA--CGTTTCGACAACT 307
DB 267 CGCGTGTGATCTTCGCGCTGCTGATTCGCAAGAAAGGCGATCATCAGGTGAGAACT 326
QY 308 ACATTATGCAATTAACCACTTTCGCAAGAGAGCTGCGCTTATCGGGGATAG 367
DB 327 ACTGCGCGCACCAAGCTGTCGCGCAACCTGCGCGCTGCTGCTGCGCAAGCAAG 386
QY 368 AGTGAACAAACGTTTGAAGAACGCGCAAGTAATCAAGTACGCTGCTCCGCGCTCG 427
DB 387 AGCTGACGAGATGCTGCGCGAGCGCGCGCTGAACTGGAATCAAGCAAGTCTCG 446
QY 428 ATGAAGCGCGCGGCTTGGGCTGTAAGTCTTCGTTACGAATCAAGATTTGGTTTC 487
DB 447 ATGCGCAACCGACGCGCTGCGGCGATCAAGGTCGGAATGTAAGATCAAGCAAGTCTGATC 506
QY 488 CGCGCAAGAAATCTTCGCGCAT 512
DB 507 TCAACGAATGATGTTGCGCAT 531

RESULT 15
US-09-621-976-1043
Sequence 1043, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1043
LENGTH: 532
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 363..530
US-09-621-976-1043

Query Match 7.4%; Score 70.4; DB 4; Length 532;
Best Local Similarity 51.1%; Pred. No. 5e-11;
Matches 187; Conservative 1; Mismatches 177; Indels 1; Gaps 1;

QY 62 TCATCCCGAGAGAGAGGTCAGGTTGTCGAAAGGCTGGGGGTTTCATCGGCGCTTA 121
DB 153 TGTGTCGCGAGAGAGGCTGGGGTGTGAGCGAATGGCGCATTCACCGGATCTGG 212
QY 122 CGGCGGTTGGAATTTTGAATTCCTTTATCGACCGCGT-CGCTACCGCGAATTCGCTG 180
DB 213 ACCCTGTTGAACATTCCTCATCCGTGTATASACCGGATCCGATATGAGAGTCTC 272
QY 181 AAGAAGTCCCTTGAAGCTTACCGACCGAGTCTGATCAACGCGCATTAATACGAATTG 240
DB 273 AAGGAATTTGTCATCAACGCTGCTGAGCAGTCCGCTGTGATCTCACAATGTAACTCTG 332
QY 241 ACTGTTGAGGAGATCATTAATTTCCAGTAACGATCCAACTGCGCTCATACGCTTG 300
DB 333 CAATTCGATGAGTCTCTTAACCTGCGCATATGAGACCTTTACAGGCAAGCTACGCTG 392
QY 301 AGCACTACATTAATGAGCAATTAACCGAGCTTGCCCAACGACGCTGCTTCCGTTACG 360
DB 393 GAGGACCCGAGATGATCCCTGACCCGAGTACGTAACAACATGATCAGAGCTCGG 452
QY 361 CGTATGAGTGGACAAAAGTTTGAAGAACGACGAAATCAACATACGCTGCTCTCC 420
DB 453 AAACCTCTCTGACAAAGCTTCCGGGGAACGAGTCCCTGAATCCGACATTTGAGAT 512
QY 421 GGCCTC 426
DB 513 GCCATC 518

RESULT 16

US-09-248-796A-2756
; Sequence 2756, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2756
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2756

Query Match 6.8%; Score 64.8; DB 4; Length 840;
Best Local Similarity 48.4%; Pred. No. 3e-09;
Matches 211; Conservative 0; Mismatches 222; Indels 3; Gaps 1;

QY 65 TCCCCAGAGAGATTCAGCTTGTGCAAAAGCTCGGGCGTTTCATCGCGCCCTGACGG 124
DB 359 TACCAAGAGAGAGCTGGATAGTAAAGAAATGGGTAGTTCCATCGTATTTGCTC 418
QY 125 CCGCTTGAATTTTGAATTCCTTTATCGACCGCGCTACCGCATTCGCTGAAG 184
DB 419 CTGATTAAGTATTTTGAATTCCTTTATTAATAAGTTAATGTTCAAAATTTAAG 478
QY 185 AATCCCTTGAAGTATTCAGGCTGATCAACGCGCATTAATACGAATGAGCTG 244
DB 479 AATGCGATTAAGATTAACATTAACAAGATCTATTAATGATTAATGATAAATTAAT 538
QY 245 TTGACGCGATCATTAATTTCAAGTAACGATCCCAAACTCGCTCATACGTTCAAGCA 304

DB 539 TAAATGATTAATTAATTAATAATCATTAATCCATTAATAAGCAAGTATGAAATTGACG 598
QY 305 ACTACATTAATGCAATTAACCAAGCTTGCCCAAGACAGCTGCTCCGTTATCGGCGCA 364
DB 599 ATTATTAATTAATTAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 658
QY 365 TCGAGTTGAGCAAAAGCTTGAAGAGCGACGAATCAACAGTACCGTCTCGGCC 424
DB 659 TAGAATTAATCGAAATTTTGAATAATCGGAATTAATTAATTAATTAATTAATTAATTA 718
QY 425 TCGATGAAGCCCGCGG---CTTGCGGTGTGAAGTCTCTCGTTACGAATCAAGATT 481
DB 719 TTAATGAAGCAATGAGAAATTTGGGGATTGAATGATTAATTAATTAATAAGATA 778
QY 482 TCGTCCGCGCAAG 497
DB 779 TTATCCCAACACAAA 794

RESULT 17

US-09-252-991A-5903
; Sequence 5903, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5903
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5903

Query Match 6.2%; Score 59; DB 4; Length 546;
Best Local Similarity 51.3%; Pred. No. 1.4e-07;
Matches 137; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 304 AACTACATTAATGCAATTAACCAAGCTTGCCCAAGACGCTGCTTCGTTATCGGGCGT 363
DB 64 AACTACCTGCGCGCACAGCCAGTGTGGCCAGAACCACTCGCGGCTGCGGCAAG 123
QY 364 ATGAGTTGACAAAAGTTTGAAGAACGCAAGAAATCAACATACGCTGCTCTCGCC 423
DB 124 CACGAGCTGACAGATGCTCGCCGAGCGCGCTCAACCTGATTAACGCAAGT 183
QY 424 CTGATGAAGCCCGCGGCTTGAGAGTGAAGTCTCGTTACGAATCAAGATTG 483
DB 184 CTGATGCGCAGACGACGCTGCGCATCAAGTGGCAATGGAATCAAGCAGT 243
QY 484 GTTCCGCGCAAGAAATCTTCCGCAATGACGCAATTAACCGCAAGCGCAAAA 543
DB 244 GATTCGAAGATCATGATGTTGCGGCATCGCCGCGCAGCGGAGCGTGAAGCG 303
QY 544 CGGCGCGTATTCGCAATCCGAAGC 570
DB 304 AGGCGCAAGTATCATCCAGAGGC 330

RESULT 18

US-09-252-991A-5987/c
; Sequence 5987, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 5987
;; LENGTH: 648
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5987

Query Match 6.2%; Score 59; DB 4; Length 648;
Best Local Similarity 51.3%; Pred. No. 1.5e-07;
Matches 137; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

OY 304 AACTACATTATGCGCAATTACCGAGCTTGCCCAAGACGCGTCCGTTATCGGGCGT 363
DB 588 AACTACCTGCGCGCCGACCAAGCGGTTGGCCCAACCACTGCGCGCGCTGCGGCAAG 529
OY 364 ATGAGTTGACAAACGTTTGAAAGACGCGAAGAAATCAACAGTACCGTCTCCGCC 423
DB 528 CACGAGCTGACAGAGATGCTGCGCGAGCGCGCTGAACCTGATATCCAGCAAGTG 469
OY 424 CTCGATGAAGCCCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATTG 483
DB 468 CTCGATGCGAGACCGAGCGCTGGGGCATCAAGTGGCAATGTGAAATCAAGACGTC 409
OY 484 GTTCCGCGCAAGAAATCTTCCGCGCAATGACGAGCAAAATTAACGCCGCAAGAAA 543
DB 408 GATCTCAACGAATCATGATGTTGCGCCCATCGCCCGGACGCGGAGCGGAGCGTGAAGCC 349
OY 544 CGCGCCCGTATTCGGAATCCGAAAGC 570
DB 348 AGGCGCAAGTGATCCATCGCGAGGCG 322

RESULT 19
US-09-270-767-13578
; Sequence 13578, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13578
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-13578

Query Match 6.2%; Score 58.8; DB 4; Length 1338;
Best Local Similarity 47.0%; Pred. No. 2.4e-07;
Matches 180; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

OY 188 TCCCTTAGACGATCCAGCGAGTCTGCATCAGCGGATTAATACGAATTGACTGTG 247
DB 687 TCTCTTAGACGATCCAGCGAGTCTCTCAAGAACTCGGTACTGTGACGCTAG 746
OY 248 ACGGATATCTATTTCCAGTAAGTCCGAATCTGCCCTCATACGTTGAGCAACT 307
DB 747 ATGCGGTGCTACTACGCAATCAGGATCCCTCAAGGCGGTATCCAGGTTGCAAT 806

OY 308 ACATTATGCAATTACCAAGCTTGCCCAAGACGCTGCGTTCCGTTATCGGGCGTATG 367
DB 807 ACAGCAATTCAGCAAGTCTCTGCGGCGCACACGATGCGCAATGTGCTCGGCACAGAA 866
OY 368 AGTTGACAAACGTTGAAGACGCGAAGAAATCAACAGTACCGTGTCTCCGCCCTCG 427
DB 867 ATCTGTCCGAGCTCTGACCGAAGCAGACATCTGCACACCATGAGATGTCTCTCG 926
OY 428 ATGAAGCGCGCGGGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATTGTTG 487
DB 927 ACNAGGCCACCGATCTCTGGGGCTTAAAGTGAAGCCGCTGGAATCAAGACATTCCT 986
OY 488 CGCGCAAGAAATCTTTCGCAATGCAAGCAAAATTAACCGCGAAGCGAAAAAGCG 547
DB 987 TGCCAATGCTCTCAGGCGGCGATGCGCGGAGGAGGAGGAGGAGGCGGCGG 1046
OY 548 CCCGATTCGCAATCCGAAGGC 570
DB 1047 CCAAGTCAATTGCGCGAGGCG 1069

RESULT 20
US-09-270-767-15253/C
; Sequence 15253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15253
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15253

Query Match 6.1%; Score 58; DB 4; Length 420;
Best Local Similarity 52.5%; Pred. No. 2.4e-07;
Matches 127; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

OY 328 CTTCGCCAAAGACGCTGCGTTCCGTTATCGGGGTAATGAGTTGACAAACGTTGAA 387
DB 374 CTGGACAGATATCTTACAGAGGACAAATGGAATCGGACATTTGATGATATCTGAC 315
OY 388 GAAGCGACGAATCAACAGTACCGTGTCTCCGCCCTCGATGAAGCCCGGGGCTTGG 447
DB 314 GAGGATATGACGATTTCCGACAAATGCAAGTTCACTGACGAAGCCACCGATGCCCTG 255
OY 448 GGTGGAAGTCTCCGTTACGAATCAAGATTGTTCCGCCGCAAGAAATCTTCCG 507
DB 254 GGCATCAAGTTGAACGTTGGAATCAAGGTCTGCTGCTGCGGCGCACTCAAGCT 195
OY 508 GCAATGACGACAAATTAACCGCGAAGCGCAAAAAAGCGCCGATATTCGAATCCGAA 567
DB 194 GCAATGCGCGGAGGAGCAAGAGCCCGGGAAGCCCGGCAAGTCAATGCGCGCGAA 135
OY 568 CG 569
DB 134 GG 133

RESULT 21
US-09-222-575-26/C
; Sequence 26, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Xugu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqun

```

; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-26

Query Match
5.7%; Score 53.8; DB 3; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCCGATCAACCGCCGCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTGCATTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCGAAGCCATCCGTCAATTCGCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGCAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGGAACAATAGTACCGGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGACGGCGCTTCCAA 1

RESULT 22
US-09-389-681-26/c
; Sequence 26, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-26

Query Match
5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCCGATCAACCGCCGCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTGCATTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCGAAGCCATCCGTCAATTCGCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGCAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGGAACAATAGTACCGGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGACGGCGCTTCCAA 1

Query Match
5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCCGATCAACCGCCGCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTGCATTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCGAAGCCATCCGTCAATTCGCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGCAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGGAACAATAGTACCGGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGACGGCGCTTCCAA 1
```

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DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGACGGCGCTTCCAA 1

RESULT 23
US-09-620-405B-26/c
; Sequence 26, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-26

Query Match
5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCCGATCAACCGCCGCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTGCATTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCGAAGCCATCCGTCAATTCGCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGCAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGGAACAATAGTACCGGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGACGGCGCTTCCAA 1

RESULT 24
US-09-339-338-26/c
; Sequence 26, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-26

Query Match
5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCACATCCGAAGCGGCTCAGGCTCGGTCAATGCGTCCAT 666
DB 233 CGAGAGTGGCCATCATGTGGCAGAGGAGAAACAGGCCAGATCTGCTCCGAA 174
QY 667 GCCGAAATGCGCCGATCAACCGCCGCAAGGCGAAATCCCTGCGCTTGT 726
DB 173 GCAGAAAGGCTGCACATTAATAGGACAGAGAGGCCAGTGCATTTCTGGCGAAG 114
QY 727 GCCGAAGCCAAATGCGAAGCCATCCGTCAATTCGCGCCCTTCAACCCAGGCGG 786
DB 113 GCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGCAGCTCTGACACACATATATGA 54
QY 787 GCGGATGCGGTCAATCTGAAGTTGGGGAACAATAGTACCGGCTTCAACA 839
DB 53 GATGAGCAGCTTCACTGACTGTGGCCGAGCAGTATGACGGCGCTTCCAA 1
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Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGAGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAAAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGCAAGGCGAAGCGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCGCAGTGTGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCCAAATGCCGAAGCCATCCGTCAATGCCCCGCCCTTCAAAACCAAGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTAAGCTATTGCAATCTGGCTGCACTTGCACAACTAATGGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 787 GCGGATGCGTCAATCTGAAGATTGCGGAACATATCGTAGCCGCGTTCACAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 GATGACAGAGCTTCACTGACTGTGGCCGACAGCATATGTCAAGCGCTTCCAA 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 25

US-09-433-826B-26/c

; Sequence 26, Application US/09433826B
; Patent No. 6579973

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqi

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jianshun

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; FILE REFERENCE: 210121.470C4

; CURRENT APPLICATION NUMBER: US/09/433,826B

; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 474

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-433-826B-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGAGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAAAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGCAAGGCGAAGCGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCGCAGTGTGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCCAAATGCCGAAGCCATCCGTCAATGCCCCGCCCTTCAAAACCAAGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTAAGCTATTGCAATCTGGCTGCACTTGCACAACTAATGGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 787 GCGGATGCGTCAATCTGAAGATTGCGGAACATATCGTAGCCGCGTTCACAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 GATGACAGAGCTTCACTGACTGTGGCCGACAGCATATGTCAAGCGCTTCCAA 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 26

US-09-604-287A-26/c

; Sequence 26, Application US/09604287A
; Patent No. 6586572

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqi

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jianshun

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7

; CURRENT APPLICATION NUMBER: US/09/604,287A

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 489

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-604-287A-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGAGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAAAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGCAAGGCGAAGCGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCGCAGTGTGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCCAAATGCCGAAGCCATCCGTCAATGCCCCGCCCTTCAAAACCAAGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTAAGCTATTGCAATCTGGCTGCACTTGCACAACTAATGGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 787 GCGGATGCGTCAATCTGAAGATTGCGGAACATATCGTAGCCGCGTTCACAA 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 GATGACAGAGCTTCACTGACTGTGGCCGACAGCATATGTCAAGCGCTTCCAA 1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 27

US-09-285-480-26/c

; Sequence 26, Application US/09285480
; Patent No. 6590076

; GENERAL INFORMATION:

; APPLICANT: Yuqi, Jiang

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Xu, Jianshun

; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; FILE REFERENCE: 210121.470C1

; CURRENT APPLICATION NUMBER: US/09/285,480

; CURRENT FILING DATE: 1999-04-02

; NUMBER OF SEQ ID NOS: 181

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 301

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-285-480-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Oy 607 CGTGAAGCCGAATCCAAATCCGAGGCGAGCTCAGGCTGCGTCAATGCGTCCAT 666
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 CGAGAGTGGCCATCAATGTGGCAGAAAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 667 GCCGAGAAATCGCCCGCATCAACCGCCGCAAGGCGAAGCGAATCCCTGGCCTTGT 726
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 GCAGAAAAGGCTGCACAGATTAATCAGGACAGAGAGGCGCAGTGTGCGAAG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 727 GCCGAGCCAAATGCCGAAGCCATCCGTCAATGCCCCGCCCTTCAAAACCAAGCGGG 786
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 GCCAAGGCTAAAGCTAAGCTATTGCAATCTGGCTGCACTTGCACAACTAATGGA 54
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

QY 787 GCGGATGCGTCAATCTGAAGATTGCGGAACAATAGTAGCCGCGTTCACAA 839
Db 53 GATGACGACGCTTCACTGACTGTGGCCGACGAGTATGTCAAGCGCGTTCCTCCAA 1

RESULT 28

US-09-834-759-26/c
; Sequence 26, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-834-759-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCAAATCCGAAGCGGCTCAGCTGCGGTCAATCGTCCAT 666
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
QY 667 GCCGAAATGCGCCGATCAACCGCGCAAGGCGAAATCCCTGCGCTTGT 726
Db 173 GCAGAAAGGCTGCACAGTAATATCAGCAGCAGGAGGCCAGTCACTTGGCGAG 114
QY 727 GCCGAAGCCATGCGGAGCCATCCGTCAATTCGCCGCCCTTAAACCAAGCGG 786
Db 113 GCCAAGGCTAAAGCTAAGCTATTCGAATCTGCTGCGAGCTCTGACACAATATATGA 54
QY 787 GCGGATGCGTCAATCTGAAGATTGCGGAACAATAGTAGCCGCGTTCACAA 839
Db 53 GATGACGACGCTTCACTGACTGTGGCCGACGAGTATGTCAAGCGCGTTCCTCCAA 1

RESULT 29

US-09-590-751A-26/c
; Sequence 26, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C6
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-751A-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCAAATCCGAAGCGGCTCAGCTGCGGTCAATCGTCCAT 666
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
QY 667 GCCGAAATGCGCCGATCAACCGCGCAAGGCGAAATCCCTGCGCTTGT 726
Db 173 GCAGAAAGGCTGCACAGTAATATCAGCAGGAGGCGCAATGCTTGGCGAG 114
QY 727 GCCGAAGCCATGCGGAGCCATCCGTCAATTCGCCGCCCTTAAACCAAGCGG 786
Db 113 GCCAAGGCTAAAGCTAAGCTATTCGAATCTGCTGCGAGCTCTGACACAATATATGA 54
QY 787 GCGGATGCGTCAATCTGAAGATTGCGGAACAATAGTAGCCGCGTTCACAA 839
Db 53 GATGACGACGCTTCACTGACTGTGGCCGACGAGTATGTCAAGCGCGTTCCTCCAA 1

RESULT 30

US-09-551-621-26/c
; Sequence 26, Application US/09551621
; Patent No. 6825175
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C5
; CURRENT FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-551-621-26

Query Match 5.7%; Score 53.8; DB 4; Length 301;
Best Local Similarity 51.9%; Pred. No. 3.8e-06;
Matches 121; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 607 CGTGAAGCCGAATCCAAATCCGAAGCGGCTCAGCTGCGGTCAATCGTCCAT 666
Db 233 CGAGAGTGGCCATCAATGTGGCAGAGGAAAGAAACAGGCCAGATCTGGCTCCGA 174
QY 667 GCCGAAATGCGCCGATCAACCGCGCAAGGCGAAATCCCTGCGCTTGT 726
Db 173 GCAGAAAGGCTGCACAGTAATATCAGCAGCAGGAGGCCAGTCACTTGGCGAG 114
QY 727 GCCGAAGCCATGCGGAGCCATCCGTCAATTCGCCGCCCTTAAACCAAGCGG 786
Db 113 GCCAAGGCTAAAGCTAAGCTATTCGAATCTGCTGCGAGCTCTGACACAATATATGA 54
QY 787 GCGGATGCGTCAATCTGAAGATTGCGGAACAATAGTAGCCGCGTTCACAA 839
Db 53 GATGACGACGCTTCACTGACTGTGGCCGACGAGTATGTCAAGCGCGTTCCTCCAA 1

RESULT 31

US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bull et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocox

```
Patent No. 6503729
TITLE OF INVENTION: jannaschi
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschi
FEATURES:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (312993)..(312993)
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OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (674435)..(674435)
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (106846)..(106846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
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/ NAME/KEY: misc.feature
/ LOCATION: (1349473)..(1349473)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1349491)..(1349491)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1470091)..(1470091)
/ OTHER INFORMATION: n equals a, t, c, or g
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/ LOCATION: (1569020)..(1569020)
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/ LOCATION: (1602912)..(1602912)
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/ LOCATION: (1603734)..(1603734)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1637998)..(1637998)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
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/ OTHER INFORMATION: n equals a, t, c, or g
/ US-08-916-421B-1

Query Match      5.4%; Score 51; DB 4; Length 1664976;
Best Local Similarity 46.0%; Pred. No. 0.0014;
Matches 172; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 196 GACGATCCAGCCAGGCTGTCATCAGCCGCGATATACCGCAATTGACTGTTGACGGCATC 255
DB 724286 GATATCCCTCTCCAGAGATGATTTACAAAGATTAATGCAATTGTAAGGATGCGGTT 724227
QY 256 ATCTATTTCCAAAGTACCGATCCCAATCGCTCTCACTAGCGTTCGAGCACTACATTATG 315
DB 724226 GTTTATTAATAGGTTTAATGATTTGTAAGGCAATTTAGAACTTGAGATTTAGCAAT 724167
QY 316 GCATATCCAGCTTCCCAAAAGAGCTGCTCCGTTACGGCGATGAGATTGAGC 375
DB 724166 GCTATTAATACTTAGCTCAACCACTAGAGGCAATATTTGTAATGAGTTAGAT 724107
QY 376 AAAACGTTGAAGAACGCGAGCAATCAACAGTACCGTCTCCGCCCTCGATGAAGCC 435
DB 724106 GAGGTTTAAATTAAGGAGTATATAAAGTTAACTCAAGTTATGGAATTTTGTAGAG 724047
QY 436 GCCGGGGCTTTGGGGGTGGAAGTCTCCGTTAGAAATCAAGATTGTTCCGGCGCA 495
DB 724046 ACGATGCAATGGGAGTTAGATTGAAAGTTGAAAGTTAAAGTTAAAGTAAAGTAA 723987
QY 496 GAAATCCTTCGCGCATGACGAGCAAAATTACCGCGAAGCGCAAAACGCCCGTAT 555
DB 723986 GACATTAAAAATCCATGCTCAACAAATGAAGGAGAGGATTTGAAGAGAGCAAT 723927
QY 556 GCCGAATCCGAGG 569
DB 723926 TTAGAGCAGAGG 723913

RESULT 32
US-09-692-570-1/c
/ Sequence 1, Application US/09692570
/ Patent No. 6797466
/ GENERAL INFORMATION:
/ APPLICANT: Bult et al.
/ TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
/ Patent No. 6797466
/ TITLE OF INVENTION: jamaeschii
/ FILE REFERENCE: PB275C1
/ CURRENT FILING DATE: 2003-01-14
/ PRIOR APPLICATION NUMBER: US 60/024,428
/ PRIOR FILING DATE: 1996-08-22
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/ PRIOR APPLICATION NUMBER: US 08/916,421
/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1664976
/ TYPE: DNA
/ ORGANISM: Methanococcus jamaeschii
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (28222)..(28222)
/ OTHER INFORMATION: n equals a, t, c, or g
/ FEATURE:
/ NAME/KEY: misc.feature
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/ OTHER INFORMATION: n equals a, t, c, or g
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/ NAME/KEY: misc.feature
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/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (231980)..(231980)
/ OTHER INFORMATION: n equals a, t, c, or g
/ FEATURE:
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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NAME/KEY: misc feature
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FEATURE:
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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Query Match 5.4%; Score 51; DB 4; Length 1664976;
Best Local Similarity 46.0%; Pred. No. 0.0014;
Matches 172; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

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QY 196 GACGTACCCAGCCAGCTGTCATCAGCGGCATATACGCAATTGACTTTGACGGCATC 255
DB 724286 GATATCCCTCCTCAAGAGATGATTAACAAGATATGCAATTGTGMAAGTGATGCGGTT 724227
QY 256 ATCTATTTCCAAAGAACGATCCCAAACTGCTCATACGGTTCGACATCATATTATG 315
DB 724226 GTTATTTATAGGGTTATATAGATTGMAAAGCAATTTTGAAGTTGAGATTACGAATAT 724167
QY 316 GCAATTACCCAGCTTGGCCCAACGACGCTGCTCCGTTATCGGCGGTATGAGTTGAC 375
DB 724166 GCTATATTAATTAAGTCAACCAACCACTGAGGCAATTAATGTGATGAGATTGAT 724107
QY 376 AAAACGTTGAAGAACGCGACGAATCAACATGATCCGTGCTCCGCCCTCGATGAAGCC 435
DB 724106 GAGCTTTTAATTAAGGAGGATATTAACCAAGTTATGMAATTTGGATGAGAG 724047
QY 436 GCCGGGCTTGGGGTGGAAGTCCTCCGTTAAGAAATCAAGATTTGGTTCCGCCGCA 495
DB 724046 ACAGATGATGGGAGATTAGAGTTGAAAAGGTTGAAGTAATGACCCACAGAG 723987
QY 496 GAAATCCTTCCGCAATGCAAGGCAAAATTACCGCCGACGCAAAAACGCCCGCTGATT 555
DB 723986 GACATTAATAATGCAATGCTCAACCAATGAGGACAGAGATTGAGAGAGGACGATA 723927
QY 556 GCCGATTCGGAAG 569
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FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9
LENGTH: 982
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 72..944
NAME/KEY: sig_peptide
LOCATION: 72..197
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 7.1999980926514
OTHER INFORMATION: seq ILFSLFLVIT/FP
US-09-621-976-9

Query Match 5.2%; Score 49.2; DB 4; Length 982;
Best Local Similarity 49.6%; Pred. No. 0.00016;
Matches 126; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 316 GCAATTACCCAGCTTGCCCAACGACGCTGCTCCGTTATCGGGCGTATGAGATTGAC 375
DB 486 GCAACATTTCTGCTGGCTCAACACACTCTGAGAAATGCTTAGGACACAGACCTTGTC 545
QY 376 AAAAGCTTGAAGAACGGACGAATCAACGATACCGTCTCTCCGCCCTCGATGAAGCC 435
DB 546 CAGATCTTAGCTGACGAGAAAGATCGCCATCACTTCAGACTTTTACTTGATATATCC 605
QY 436 GCCGGGGCTTGGGGTGAAGTCTCCTCGTTACGAATCAAGATTTGGTCCCGCAA 495
DB 606 ACCGACCTGTGGGGATCCGGTGGCCCGAGTGAATCAAGATTTGGATTCGGTG 665
QY 496 GAAATCTTCCGCGAATGACGACAAATTACCGCGAAGCGGAAACGGCCCGTATT 555
DB 666 CAGTTGACAGATCCATGCGACGCGAGCTGAGCCACCCGGAGACGAGCCAAAGTTC 725
QY 556 GCCGAATCCGAAG 569
DB 726 CTGCACTGAAG 739

RESULT 36

US-09-663-600A-60
Sequence 60, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duciart, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 60

LENGTH: 1022
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 112..237
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 7.1999980926514
OTHER INFORMATION: seq ILFSLFLVIT/FP
NAME/KEY: polyA_signal
LOCATION: 976..981
NAME/KEY: polyA_site
LOCATION: 1010..1022
US-09-663-600A-60

Query Match 5.2%; Score 49.2; DB 4; Length 1022;
Best Local Similarity 49.6%; Pred. No. 0.00016;
Matches 126; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 316 GCAATTACCCAGCTTGCCCAACGACGCTGCTCCGTTATCGGGCGTATGAGATTGAC 375
DB 526 GCAACATTTCTGCTGGCTCAACACACTCTGAGAAATGCTTAGGACACAGACCTTGTC 585
QY 376 AAAAGCTTGAAGAACGGACGAATCAACGATACCGTCTCTCCGCCCTCGATGAAGCC 435
DB 586 CAGATCTTAGCTGACGAGAAAGATCGCCATCACTTCAGACTTTTACTTGATATATCC 645
QY 436 GCCGGGGCTTGGGGTGAAGTCTCCTCGTTACGAATCAAGATTTGGTCCCGCAA 495
DB 646 ACCGACCTGTGGGGATCCGGTGGCCCGAGTGAATCAAGATTTGGATTCGGTG 705
QY 496 GAAATCTTCCGCGAATGACGACAAATTACCGCGAAGCGGAAACGGCCCGTATT 555
DB 706 CAGTTGACAGATCCATGCGACGCGAGCTGAGCCACCCGGAGACGAGCCAAAGTTC 765
QY 556 GCCGAATCCGAAG 569
DB 766 CTGCACTGAAG 779

RESULT 37

US-09-252-991A-6989
Sequence 6989, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6989
LENGTH: 1602
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6989

Query Match 4.5%; Score 42.4; DB 4; Length 1602;
Best Local Similarity 46.8%; Pred. No. 0.0022;
Matches 133; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 439 GGGGCTTGGGGTGAAGTCTCCTTACGAATCAAGATTGTTCCGCCCGAAGAA 498
DB 1165 GCAACCTACGGGGTCAAGGTGTGAGTGGCATGACGCGCTGACCCCTCCAAAGGTG 1224
QY 499 ATCTTGGCGCAATGACGACCAATTAACCGCCGAGCGGAAAAACGGCCCGATTGCC 558
DB 1225 ACCCTGGCGCACCGTGAACCGATGGCGCCGAGGCGGAGACCATCGCACGAGCGT 1284

QY 559 GAATCCGAGCGGCTAAATTCGAACAATCACTTCCAGTGTGAGGCGGAA 618
| | | | |
DB 1285 ACCGCGGAGCGGCTGCGGAGATCCGTTCCGCGCGGAGCGCGCGG 1344
| | | | |
QY 619 ATCCAAATCCGAGGCGGCTGAGGCTGCGTCAATGCGCAATCCGAGAAATC 678
| | | | |
DB 1345 GTGATCAGGCGGAGGCTTCCGTGAAAGCCGCGAATGAGGCCCGAGGCTTCAG 1404
| | | | |
QY 679 GCCCGCATCAACGCGCGCAAGGCGGAAATCCCTGCGCCT 722
| | | | |
DB 1405 GCGGCGGATCTACGCGCAAGGCTTCCGCGGCTTCCGCGAGCT 1448
| | | | |

RESULT 38
US-09-252-991A-7042
; Sequence 7042, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7042
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7042

Query Match 4.5%; Score 42.4; DB 4; Length 2187;
Best Local Similarity 46.8%; Pred. No. 0.025;
Matches 133; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 439 GGGGCTTGGGGGTGGAAGCTCCGTTACGAATCAAGATTGTTCCGCGCAAGAA 498
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DB 92 GCGACCTACGGGTCAAGGTGTGCAAGTGTGCGATGCGCTTACCTCCCAAGTGC 151
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QY 499 ATCTTTCGCGCAATGCAAGCAAAATTAACCGCGAAACGCGAAACGCGCGTATTGCC 558
| | | | |
DB 152 ACCCTCGCGCCACCGTCGACCGCATGCGCGGAGCGGAGCAATCGCACGAGCT 211
| | | | |
QY 559 GAATCCGAGGCGGTAAATCGAACAATCACTTCCAGTGTGAGGCGGAA 618
| | | | |
DB 212 ACCGCGGAGGCGGCTGCCAGCTGCGGAGATCCGTTCCGCGCGGAGCGCGCGG 271
| | | | |
QY 619 ATCCAAATCCGAGGCGGAGGCTCAGGCTGCGTCAATGCGCAATGCGGAAATC 678
| | | | |
DB 272 GTGATCAGGCGGAGGCTTCCGTGAAAGCCGCGAATGAGGCCCGAGGCTTCAG 331
| | | | |
QY 679 GCCCGCATCAACGCGCGCAAGGCGGAAATCCCTGCGCCT 722
| | | | |
DB 332 GCGGCGGATCTACGCGCAAGGCTTCCGCGGAGCT 375
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RESULT 39
US-09-221-017B-544
; Sequence 544, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 544:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1...503
US-09-221-017B-544

Query Match 4.3%; Score 41.2; DB 3; Length 503;
Best Local Similarity 55.6%; Pred. No. 0.03;
Matches 79; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 626 AATCCGAGGCGAGGCTGAGGCTGCGTCAATGCGCGGAGAAATCGCCGCA 685
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DB 5 AATCGAGGCTAAGTCAAGGAGTCCATCAACAGCTGAGGAGGAGGAGCGGCGAAG 64
| | | | |
QY 686 TCAACCGCGCCAAAGCGGAGGAAATCCCTGCGCCTTTTGTCCGAGCAATGCCGAAG 745
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DB 65 TTCTCAGAGCCAAAGCTGAGGCAAGGCTAAGATTTGTTGCTCAAGGCGAGGCCGAAAG 124
| | | | |
QY 746 CCATCGTCAATGTCGCGCGC 767
| | | | |
DB 125 CTATCCGCAATGAGCGAAGC 146
| | | | |

RESULT 40
US-08-181-271A-106
; Sequence 106, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Spertson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Unnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-181-271A-106

Query Match 4.3%; Score 41; DB 1; Length 1031;
Best Local Similarity 48.1%; Pred. No. 0.047;
Matches 116; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

Qy	365	TGAGCTTGACAAACGTTTGAAGACCGACGAAATCAAGTACCGTCTCCGCC	424
Db	390	TGAACCTGGACGATGTTCAGCGAAGATGAATTCCTGTGGAAGAAGAC	449
Qy	425	TCGATGAAGCCGCGGCTTGAGGATGAAGTCTCCGTTACGAATCAAGATTGG	484
Db	450	TAGACAAAGCCATGACGTCTTATGTACGAAATCCTTCAACCTTAATTGACATTG	509
Qy	485	TTCCGCCGCAAGAAATCCTTCGCGCAATGCAGCACAAAATTACCGCGAAGCGAAAAAC	544
Db	510	AGCTGATCAACAGATTAAACGTCCATGAACGAAATCAACGCCGCGGAGATGAGAG	569
Qy	545	GCGCCCGATATGCCGAATCCGAAGCCGTAAATCGAAACAAATACCTTGCCAGTGC	604
Db	570	TGGCAGCGAGCAAAAGACAGAGGCTGAGAAATCATTCAGATCAAAAGACAGAGGTG	629
Qy	605	A 605	
Db	630	A 630	

Search completed: August 14, 2005, 01:49:39
Job time : 227 secs


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OY 120 GACGCGCGATTTGAATATTTTATCCCTTATCGACCGCGCTACCGCATTCGCT 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 397 CGGCTCCGGGTTCCACCTCTGATCCCGCGCTGACCGTATGCTTACGTGCACTGCT 456
OY 180 GAAAGAAATCCCTTTAGACGTAACCGACGAGTGTGATCAAGCGCGATTAATACGCAAT 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 457 CAAGGAGAGACATCCCTATCCCTACACAGAACCGCATCAAGAGAACAGTCAACAT 516
OY 240 GACTTTGACGCGATCTATTTTCCAGTAAACGATCCCAACCTCGCTCATACGCTC 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 517 ACAGATTGACAGCGCTATCTATGTCAAGATCGATGAGATCAATTAATGAGAAATTTGTAG 576
OY 300 GAGCACTACATTAATGCAATTAACCGAGCTTGCAGCAACGAGCTGCTGCTTATGCT 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 577 GAGAAATCCATCTATGCTGTCTCAACATTCGACAAACACATGAGAAAGTAACTGG 636
OY 360 GCGTATGAGATTGACAAACGTTTGAAGAACGCGACGCAATCAACAGTACCGTGTCTC 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 637 GAAATTAACCTTAGATTAAGACTTTTGAAGAGAGATGATCAATTAATGAGAAATTTGTAG 696
OY 420 CGCCTTCATGAAAGCGCGCGGCTTGGGGTGTGAAAGTCTCCGCTTACGAAATGCAAGA 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 697 TGCCATCAATGAGAGAGCGACAGATTGGGCGCTGAAAGTGTATCGCTATGAGATGAGGA 756
OY 480 TTTGGTCCGCGCAAGAAATCCTTCCGCAATGAGGCAACAAATTAACCGCGAAGCGGA 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 757 CATTAATCTTCAGAGAGGATTAAGCAGGCTATGAGATGAGGCTGAGGCGAAGAGAA 816
OY 540 AAAACGCGCGCTATTTCCGAAATCCGAAAGCGCGTAAATCGAAACAAATCAACTTTCGAG 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 817 AAAACGCGCTCAATCTCTTAGTCAAGAGGATGAAAC----- 854
OY 600 TGGTACGCTGAAGCGCAATTCACAAATCCGAAAGCGGCTCAGGCTCGGTGATGC 659
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 855 -----AGGCCCAATCTTTGAATCAGAAAGGAAAAAGACTGCGCAATCTTGA 903
OY 660 GTCCAATGCCGAGAAATCGCCGATCAACCGCGCAAGGCGAAGGCAATCCCTGCG 719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 904 ATCTGAAGAGATGATGTTGATCTAGCAAAACCGTGCAGAGGTGGCGCTGAAGCAATCT 963
OY 720 CTTGTTGCCGAGCAATGCCAGAACCATCCGTCAAAATGCGCGCGCTTCAAAACCA 779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 964 TGCCAATGTCAGAGCTACTGCTCGTGAATGAGATTGTTTCAGATGCGATGACAACTGA 1023
OY 780 AGCGCGGCGGATGCGGTCTCAATCTGAAGATTGCCGAAACAAATCGTACCGCTTCAAGAA 839
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1024 AGGCAGTGCGCAAGGCTGCTAGCTGAACCTTGCAAGACAAATCAATGAAACATCTCAAA 1083
OY 840 TCTTGCCAAAGAAACAAATACGCTGATTAATGCGCCCAATGTTGCC 885
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1084 TCTGCGCAAAAGACAAATACAAATGCTTCTTCAGATGATAGTGCC 1129

RESULT 2
US-10-425-115-95784
; Sequence 95784, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 95784
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Zea mays

```

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; FEATURE:
; OTHER INFORMATION: Clone ID: M8T4577_1886C.1
US-10-425-115-95784
Query Match 18.4%; Score 174; DB 20; Length 1720;
Best Local Similarity 52.4%; Pred. No. 1e-67;
Matches 433; Conservative 0; Mismatches 360; Indels 33; Gaps 1;

OY 60 CGTCATCCCCCAGAGAGAGATCCACGTTGTGAAAGGCTCGGCGGTTCCATCCGCGCT 119
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 346 CATAGTCCGAGAGAGAGGCTTACGTTGTGAGAGATTCGGAGATGATCAAGACCT 405
OY 120 GACGCGGTTGAATATTTTGAATTCCTTATTCAGCGCGGTGCTTACCGCATTCGCT 179
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 406 CGGCTCCGGGTTCCACCTCTGATCCCGCGCTGACCGTACGTAATGCTTACGCTGCT 465
OY 180 GAAAGAAATCCCTTTAGACGTAACCGACGAGTGTGATCAACGCGCGATTAATACGCAAT 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 466 CAAGGAGAGACATCCCTATCCCTCACAGAAAGCATCACAGAGCAACAGTCAACAT 525
OY 240 GACTGTGACGCGATCTATTTTCCAAATTAACCGATCCCAACTCCCTCATACGCTTC 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 526 ACAGATTGACAGCGCTCATCTATGTCAGATCATGAGACCCCTACTTGTCTTATGATGT 585
OY 300 GAGCACTCAATTAATGCGAATTAACCGCTTGCAGCAACGAGTGTGCTTATGCT 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 586 GAGAAATCAATCTATGCTGTCTTACAACTTGACAAACAAACATGAGAAAGTAACTCG 645
OY 360 GCGTATGAGATTGACAAACGTTTGAAGAACGAGAAATCAACAGTACCGCTGTCTC 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 646 GAAATTAACCTTAATTAAGACTTTTGAAGAGAGATGCAATTAATGAGAAATTTGTAG 705
OY 420 CGCCTTCATGAAAGCGCGCGGCTTGGGGTGTGAAAGTCTCCGTTACGAAATCAAGA 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 706 TGCCATCAATGAGACAGCAACAGATTGGGCTTGAATGATTCGCTATGATGATCAAGGA 765
OY 480 TTTGGTCCGCGCAAGAAATCCTTCCGCAATGAGGCAACAAATTAACCGCGAAGCGGA 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 766 CATTAATCTCTCAGCAGGATTAAGCAGGCTATGAGATGAGCTGAGCGAAGAGAA 825
OY 540 AAAACGCGCGCTATTTGCCGAAATCCGAAAGCGCGTAAATCGAAACAAATCAACTTGCAG 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 826 AAAACGCGCTCAATCTCTTAGTCAAGAGGATGAAAC----- 863
OY 600 TGGTACGCTGAAGCGCAATTCACAACTCGAAGCGAGGCTCAGGCTCGCTCAATGC 659
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 864 -----AGGCCCAATCTTTGAATCAGAAAGGAGTAAAC----- 912
OY 660 GTCCAATGCCGAGAAATCGCCGATCAACCGCGCAAGGCGAAGCGAATCCCTGCG 719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 913 ATCTGAAGAGATGATGTTGATCTAGCAAAACCGTGCAGAGGTGGCGCTGAAGCAATCT 972
OY 720 CTTGTTGCCGAAACCAATGCCAGAACCATTCCTCAAAATGCGCGCGCTTCAAAACCA 779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 973 TGCCAATGTCAGAGCTACTGCTGCTGAGATGAGATTGTTTCAGATGCGATGACAACTGA 1032
OY 780 AGCGCGGCGGATCGGCTCAATCTGAAGATTGCGAAACAAATACGTAACCGGCTTCAACAA 839
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1033 AGGCAGTGCGCAAGGCTGCTAGCTGAACCTTGCAAGACAAATCAATGAAAGATTTCTCAA 1092
OY 840 TCTTGCCAAAGAAACAAATACGCTGATTAATGCGCGCAATGTTGCC 885
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1093 TCTGCGCAAAAGACAAATACAAATGCTTCTTCAGAGTATAGTGCC 1138

RESULT 3
US-09-738-626-1692
; Sequence 1692, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO

```

```

APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO: 1692
LENGTH: 1296
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1692

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Query Match      18.1%; Score 172; DB 9; Length 1296;
Best Local Similarity 51.7%; Pred. No. 4.3e-47;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

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QY 12 CATATCTTGTGGAGCGCGTGTTCGGCTTCAATCCTTGTGTCATCCCA 71
DB 21 CATAGTTTCCGTGCTTGTGCGCGTGTGATCAATGCTCAATTCCTCA 80
QY 72 GCAGAAAGTCACGTTGTGAAGAGCTCGGCGTTTCATCGCGCTGACGCGGTT 131
DB 81 GGGTGAAGCGCGCTGATGAAAGCTTGTGATGACACCGACCGTTTCAAGTGGCT 140
QY 132 GAATATTTGATTCCTTATGACCGCGTGTGATGACCGCTTCAATGCTGTAAGAAATGCC 191
DB 141 GACCGTGTGTTCCATTCGTGACCGAGTACCGCGCAATGACACCGGTGAGCGCT 200
QY 192 TTATAGCGTACCGAGCGTGTGATGACCGCGCAATGACATGTTGATGACG 251
DB 201 GGTTCATTTCCACGCGAGCGTGTATTAACCAAGCAACCTGACCGTGCATGATAT 260
QY 252 CATCATCTATTTCAAGTAAAGATCCCAACTCGGCTCATACGTTTCAGACATACAT 311
DB 261 CGTGTGACCTTCCAAATCAAGCAACGAGCGCGCATCTACGCGTGTGACATACAT 320
QY 312 TATGCAATTAACCCAGCTTGCCTCAACGACGCTGCTTCGTTATCGGCGTATGAGATT 371
DB 321 CGTGTGTGAGAGAGATTTCTGTAGCAACTTTCAGACGTTGTGCGTGTGACCT 380
QY 372 GGAAGAAAGTTTGAAGAAAGCGAGCAATCAACATACCTGCTCGGCTTCATGATA 431
DB 381 GGAAGAAAGCTTCATCTTCAAGTGAAGTATCAACCGCGCTTCGTTGAGAGCTTCATGC 440
QY 432 AGCGCGCGGCGTGTGAGAGTGTGAAAGTCTCGTTCAAGAAATCAAGATTTGGTTCGCG 491
DB 441 AGCAACCAACCAATGAGGCGCTGTGCAATCAGCGGTGTGAACTTAAGCAATGATTCGCG 500
QY 492 GCAAGAAATCTTTCGCGCAATGACGACCAAAATTAACCGCGCAACGCGAAACGCGCGG 551
DB 501 ACCATCATCTCAGCAATTCATGTAAGAAAGAGATGAAGGACGACCGTGAAGAGCGCGCAC 560
QY 552 TATTCGCGAATCCGAAGCGCTGTAATTCGAACAAATCAACCTTGCAGTGTGTAGAGGTGA 611
DB 561 CATTTTGAACCGAGAAAGTTCAGCGCAAGCGCAATCAAACTGCGAAGTGAAGAGCA 620
QY 612 AGCGAAATTCGAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCGTCAATGCGCA 671
DB 621 AGCGAATCTCTCAAGCTGAGGATGAAGAGCAACGATCATCTCTAAGCCAGAAAGCAGA 680

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QY 672 GAAATCCCGCCATCAACCGCGCAAGCGCAAGCGAATCCTTGTGTCGA 731
DB 681 AGCGCAAGCATGATTCGCGCGCGGAGAGAGCAAGCGCAAGCGCTACAGGCGCA 740
QY 732 AGCGAATCCGAAGCGATCCTCAATTTGCGCGCG 767
DB 741 GGGTGAAGCCCGAGCAATCAAAAGTCAACGCGAGC 776

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RESULT 4
US-10-494-675-5
; Sequence 5, Application US/10494675
; Publication No. US20050019877A1

```

```

GENERAL INFORMATION:
APPLICANT: Zelder, Oskar
APPLICANT: Pompejus, Markus
APPLICANT: Schröder, Hartwig
APPLICANT: Krogger, Burkhard
APPLICANT: Klopriogge, Corinna
APPLICANT: Habermeyer, Gregor
TITLE OF INVENTION: Genes coding for metabolic pathway proteins
FILE REFERENCE: BG1-163US
CURRENT APPLICATION NUMBER: US/10/494,675
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: PCT/EP02/12141
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: DE 101 54 292.1
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 164

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SEQ ID NO 5
LENGTH: 1426
TYPE: DNA
ORGANISM: Corynebacterium glutamicum

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FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(1396)
OTHER INFORMATION: RXA00152
US-10-494-675-5

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Query Match      18.1%; Score 172; DB 21; Length 1426;
Best Local Similarity 51.7%; Pred. No. 4.5e-47;
Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

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QY 12 CATATCTTGTGGAGCGCGTGTTCGGCTTCAATCCTTGTGTCATCCCA 71
DB 121 CATAGTTTCCGTGCTTGTGCGCGTGTGATCAATGCTCAATTCCTCA 180
QY 72 GCAGAAAGTCACGTTGTGAAGAGCTCGGCGTTTCATCGCGCTGACGCGGTT 131
DB 181 GGGTGAAGCGCGCTGATGAAAGCTTGTGATGACACCGCACCGTTTCAAGTGGCT 240
QY 132 GAATATTTGATTCCTTATGACCGCGTGTGATGACCGCTTCAATGCTGTAAGAAATGCC 191
DB 241 GACCGTGTGTTCCATTCGTGACCGAGTACCGCGAAGATGACACCGGTGAGCGCT 300
QY 192 TTATAGCGTACCGAGCGTGTGATGACCGCGCAATTAATAGCAATTAATGATGACG 251
DB 301 GGTTCATTTCCACGCGAGCGTGTATTAACCAAGCAACCTGACCGTGCATGATAT 360
QY 252 CATCATCTATTTCAAGTAAAGATCCCAACTCGGCTCATACGTTTCAGACATACAT 311
DB 361 CGTGTGACCTTCCAAATCAAGCAACGAGCGCGCATCTACGCGTGTGACATACAT 420
QY 312 TATGCAATTAACCCAGCTTGCCTCAACGACGCTGCTTCGTTATCGGCGTATGAGATT 371
DB 421 CGTGTGTGAGAGAGATTTCTGTAGCAACTTTCAGACGTTGTGCGTGTGACCT 480
QY 372 GGAAGAAAGTTTGAAGAAAGCGAGCAATCAACATACCTGCTCGGCTTCATGATA 431
DB 481 GGAAGAAAGCTTCATCTTCAAGTGAAGTATCAACCGCGCTTCGTTGAGAGCTTCATGC 540
QY 432 AGCGCGCGGCGTGTGAGAGTGTGAAAGTCTCGTTCAAGAAATCAAGATTTGGTTCGCG 491

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Db 541 AGCAACCAACCAATGGGGCTGCGCATCAGCCGTGTGAACTTAAAGCAATTGATCCGCC 600
Qy 492 GCAAGAAATTCCTTGGCGAATGACAGCAAAATTATCCGCCGAAGCGAAAAACGCCGCCG 551
Db 601 ACCATCCATTCAGCATGATGAGAAAGCAATGAGGACGATCCCTGAAAAGCGGCCAC 660
Qy 552 TATTGCCGAATCCGAGGCGCGTAAATCGAACTTGGCACTGTGTGACCGTGA 611
Db 661 CATTTGACCGGAGAAAGGTGAGCGGAGCGGACATCAAACTGCCGAAGGTGAAAAGCA 720
Qy 612 AGCCGAATTCACCAATCCGAGGCGAGGCTGAGCTCGGTCAATGCTGCAATGCCGA 671
Db 721 AGCCGAATTCCTCCAGGCTGAGGCTGAAAAGCAAGCATCCATCTGAAACGAGAAAGCA 780
Qy 672 GAAATGCGCGGATCAGACCGGCGCAAGGCGGAGCGGAATCCCTGCGCTTGTGTGCCGA 731
Db 781 AGCCGAAGCATGATCTGCGCGCGCGGAGGTGAAAGCGCGAGCAGCCTTACTTCAGGCGCA 840
Qy 732 AGCCGAATGCCGAAGCCATCCGTCAATTGCGCGCGC 767
Db 841 GGGTGAAGCCGAGCATCCAAAAGTCAAGCGCAGC 876

RESULT 5
US-09-738-626-1/c

; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 18.1%; Score 172; DB 9; Length 3309400;

Best Local Similarity 51.7%; Pred. No. 2.4e-45;

Matches 391; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

Qy 12 CATATCTGTGTGAGCGCGTCCGCTTTCGCTTCAATCTTGTGTCATCCCA 71
Db 1619596 CATAGTTTTCGCGCTTGTGTGCGGTGTGTATCAAGTCCATAGCCCTGATTCCTCCCA 1619537
Qy 72 GAGGAAATCCAGCTTTCGAAAGGCTGGGCGTTTCCATGCGCCCTGAGCGCGGTTT 131
Db 1619536 GGGTGAAGCCGCGCATTTGAAGCGCTTGTGTAGTACACCGCACCGTTTCAAGTGGGCT 1619477
Qy 132 GAATATTTTGAATCCCTTATATGACGCGGCTCCACGCGCATTTGCTGAAAGAAATCC 191
Db 1619476 GACCTGCTGTTTCATTCGTCGAGTACCGCAAGATGACACCCGCTGAGCGGCT 1619417
Qy 192 TTAGAAGTACCAAGCGGCTGTGATCAGCGCGCATTAATGCAATTGACTGTGACGG 251

Db 1619416 GGTCTCATTTCCACCGCAGGCTGTATTTATCCCAAGACACTGACCGTGGCATCGATAT 1619357
Qy 252 CATCATGATTTTCCAGTAACCATCCCAATCTGCGCATATGAGTTTGAGCACTACAT 311
Db 1619356 CTGTGTGACTTCCAAATTCAGAGAACAGACCGCCCATCTTACGCGCTGAGCACTACAT 1619297
Qy 312 TATGCAATTTACCGAGCTTGGCCCAAGACGCTGCTGCTTATTCGGGCGTATGAGTT 371
Db 1619296 CGTGTGTGAGAGATTTCTGTAGCAACCTTGAGAGCTTGCGTGTGATGACCT 1619237
Qy 372 GGAAGAAAGCTTTGAGAGACGACGAAATTAAGTACGTGCTTCGCCCTTCATGA 431
Db 1619236 GGAAGAAACCTCTCACTTCACTGACGTGATCAACCGCGCTCTCGTGGCGAGTCAATGC 1619177
Qy 432 AGCCGCGGGGCTTGGGGTGTGAAAGTCTCCGTTTAAATCAAGATTTGTTCGCC 491
Db 1619176 AGCAACCAACAAATGGGGCTGCGCATGACCGGTGTGAACTTAAAGCAATTGATCCGCC 1619117
Qy 492 GCAAGAAATCCTTGGCGCATGACAGCAAAATTAACGCGCAACGCAAAACGCCGCCG 551
Db 1619116 ACCATCCATTCAGCAATGATGAGAAAGCAATGAGGACGAGTGAAGGCGGCCAC 1619057
Qy 552 TATTCCGAATCCGAGGCGGTAAATCGAACAAATCACTTGCAGTGTCAAGCTGA 611
Db 1619056 CATTTGACCGCAGAGGTCAGCGCAAGCCGACATCAAACTCCGAAGGTGAAAAGCA 1618997
Qy 612 AGCCGAATTCACCAATCCGAGGCGAGGCTCAGGCTGCGGTCAATGCTGCAATGCGCA 671
Db 1618996 AGCCGAATTCCTCCAGGTGAGGTGAAAAGCAGCATCCATCTTGAACGAGAAAGCA 1618937
Qy 672 GAAATGCGCGGATCAACCGCGCAAGGCGAAGCGGAATCCCTGCGCTTGTGTCGA 731
Db 1618936 AGCCGAAGCATGATCTCGCGCGCGGAGGTGAAGCGGACGATACCTCCAGGCGCA 1618877
Qy 732 AGCCGAATGCCGAAGCATTCGCTCAATTGCGCGCGC 767
Db 1618876 GGGTGAAGCCGAGCAATCCAAAAGTCAACGCGCAGC 1618841

RESULT 6
US-10-156-761-6459

; Sequence 6459, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6459
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(948)
US-10-156-761-6459

Query Match 17.9%; Score 169.8; DB 15; Length 948;
Best Local Similarity 53.6%; Pred. No. 2e-46;
Matches 354; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

```

QY 11 TCATTATCTGTGTGACAGCCGCGGTTTGGCTTCAAAATCTTTGTCATCCCC 70
DB 23 TGATCATCTGTGTGTGTGTGTTGCTTTCATCGCCGTGATCAAGCAATCCAGCATCCCGC 82
QY 71 AGCAGAGAGTCCAGCTTGTGCAAGAGCTCGAGGCTTTCCATCGCCCGCTGAACGCGGTT 130
DB 83 AAGCAGAGCGCGGCTTGTGAGCGCTTGTGCGGCTTCAACGCGGCTGAACGCGGCT 142
QY 131 TGAATATTTTGAATTCCTTTATCGACCGGCTGCTTACCGGCTTGTGAAAGAAATCC 190
DB 143 TGAATATGTGTGTGCTTGTGATCGATCGAAGCGGCTTGTGAAAGAAATCC 202
QY 191 CTTTGAAGTACCGACGCGCTGTGATCAAGCGGCTTGAATATCGAATGTGATGAG 250
DB 203 TCGTTCCTGTTCCTCCGCGAGCGGCTGTATCAACGAGAACTGTGTGTGATCGA 262
QY 251 GCATCATCTATTTCCAGATTAAGGATCCCAATCTGCGCTTATAGGTTGACCACTACA 310
DB 263 CGTATCTATTTATCAAGGATGACCGAGCGCGCTGCGGCTCAAGTCAAGTGTGCGCACTACA 322
QY 311 TTATGCAATTAACCGAGCTTGCCTCAACGAGCGCTGCTTGTGATGCGGCTGATGAGT 370
DB 323 TCCAGGCGATCGAGAGGCTCAACGCTCAACGCTCCGCAACATCAATCGCGGCTGAGAC 382
QY 371 TGGACAAACGTTTGAAGAGCGGAGCAATCAAGTACGCTGCTTGTGCGCTTGTGATG 430
DB 383 TGGACGCGACCTTCACTTCCCGAGAGATCAAGCGGCTTGTGCGGCTTGTGATGAG 442
QY 431 AAGCGCGCGGCTTGTGAGGCTGAAAGTCTCGCTTGAAGAAATCAAGATTTGTTGCGC 490
DB 443 AAGCGCGCGGAGTGTGAGGCTGCGGCTCAACGCTCAAGGCTCAAGGCTGAGCGC 502
QY 491 CGCAAGAAATCTTGTGCGGCTGAGGCAAGCAATTAACCGCGAGCGGCAAGCGCGC 550
DB 503 CGACCTTCATCGAGAGCTGATGAGAGCAAGTGTGCGGCTGAGCAAGCGCGC 562
QY 551 GTATTGCCGAATCCGAAGCGGCTTAAATGAACAAATCACTTGTGCGGCTGAGCGG 610
DB 563 CGATCTCACTCCGCGAGGCGGCGGCAAGCGGCTTGTGCGGCTGAGGAGAGC 622
QY 611 AAGCGGAATCCGAATCCGAAGCGGCTCAAGCTGCGGCTGATGAGGCTCAATGCGC 670
DB 623 AGTCCCAATCTGTGCGGCGGAGGAGGAGGCGGCGGCTGCGGCGGAGGCGC 682
QY 671 A 671
DB 683 A 683

```

RESULT 7
US-10-156-761-1

```

; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBATA, YOSHIO
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608

```

```

; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

```

Query Match 17.9%; Score 169.8; DB 15; Length 9025608;
Best Local Similarity 53.6%; Pred. No. 2,3e-44; Indels 0; Gaps 0;
Matches 354; Conservative 0; Mismatches 307;

```

QY 11 TCATTATCTGTGTGACAGCCGCGGTTTGGCTTCAAAATCTTTGTCATCCCC 70
DB 7760965 TGATCATCTGTGTGTGTGTGTTGCTTTCATCGCCGTGATCAAGCAATCCAGCATCCCGC 7761024
QY 71 AGCAGAGAGTCCAGCTTGTGCAAGAGCTCGAGGCTTTCCATCGCCCGCTGAACGCGGTT 130
DB 7761025 AAGCAGAGCGCGGCTTGTGAGCGCTTGTGCGGCTTCAACGCGGCTGAACGCGGCT 7761084
QY 131 TGAATATTTTGAATTCCTTTATCGACCGGCTGCTTACCGGCTTGTGAAAGAAATCC 190
DB 7761085 TGAATATGTGTGTGCTTGTGATCGATCGAAGCGGCTTGTGAAAGAAATCC 7761144
QY 191 CTTTGAAGTACCGACGCGCTGTGATCAAGCGGCTTGAATATCGAATGTGATGAG 250
DB 7761145 TCGTTCCTGTTCCTCCGCGAGCGGCTGTATCAACGAGAACTGTGTGTGATCGA 7761204
QY 251 GCATCATCTATTTCCAGATTAAGGATCCCAATCTGCGCTTATAGGTTGACCACTACA 310
DB 7761205 CGTATCTATTTATCAAGGATGACCGAGCGGCTGCGGCTCAAGTCAAGTGTGCGCACTACA 7761264
QY 311 TTATGCAATTAACCGAGCTTGCCTCAACGAGCGCTGCTTGTGATGCGGCTGATGAGT 370
DB 7761265 TCCAGGCGATCGAGAGGCTCAACGCTCAACGCTCCGCAACATCAATCGCGGCTGAGAC 7761324
QY 371 TGGACAAACGTTTGAAGAGCGGAGCAATCAAGTACGCTGCTTGTGCGGCTGATG 430
DB 7761325 TGGAGCGACCTTCACTTCCGCGAGAGATTAAGCGGCTTGTGCGGCTGATGAG 7761384
QY 431 AAGCGCGCGGCTTGTGAGGCTGAAAGTCTCGCTTGAAGAAATCAAGATTTGTTGCGC 490
DB 7761385 AAGCGCGCGGAGTGTGAGGCTTCAACGCTCAACGCTCCGCAACATCAATCGCGGCTGAGAC 7761444
QY 491 CGCAAGAAATCTTGTGCGGCTGAGGCAAGCAATTAACCGCGAGCGGCAAGCGCGC 550
DB 7761445 CGATCTCACTCCGCGAGGCGGCGGCAAGCGGCTTGTGCGGCTGAGGAGAGC 7761504
QY 551 GTATTGCCGAATCCGAAGCGGCTTAAATGAACAAATCACTTGTGCGGCTGAGCGG 610
DB 7761505 CGATCTCACTCCGCGAGGCGGCGGCAAGCGGCTTCAACGCTCAAGGCTGAGAGAGC 7761564
QY 611 AAGCGGAATCCGAATCCGAAGCGGCTCAAGCTGCGGCTGATGAGGCTCAATGCGC 670
DB 7761565 AGTCCCAATCTGTGCGGCGGAGGAGGAGGCGGCGGCTTGTGCGGCGGAGGCGC 7761624
QY 671 A 671
DB 7761625 A 7761625

```

RESULT 8

```

; Sequence 176, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARBELL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/719,993
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342

```

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-176

Query Match 17.4%; Score 165; DB 20; Length 1930;
Best Local Similarity 50.2%; Pred. No. 1.3e-44;
Matches 433; Conservative 3; Mismatches 418; Indels 9; Gaps 1;

```
QY 62 TCATCCCCCAGCAGAAAGTCCAGTGTGCGAAGGCTCGGCGTTTCCATGCGCCCTGA 121
DB 763 TCGTCCGACAGCAGAGGCTCGGTGGTGGAGCAATGCGCATTCACCGGATCCCTGG 822
QY 122 CGGCGGTTTAAATTTTGAATCCCTTATCGAACCAGGCTCAACCGCATTCGCTGA 181
DB 823 AGCTGTGTTGAACATCTCATCCCTGTGTTAGACCGGATCGAATGTGACAGTCTCA 882
QY 182 AAGAAATCCCTTGAAGCTACCCAGCCAGCTGTGATCACCGCGCATATACGCAATTGA 241
DB 883 AGGAAATTTTATATCAAGCTGCTGAGCAGTGGCTGTACTCTGACATATTAATCTGCG 942
QY 242 CTGTGACGCGCATATCTATTTCCAAAGTACCCAACTCGCTCATACGTTTGA 301
DB 943 AATTCGATGAGTCTTTACTGCGCATCATGACCCTTACAGGCAAGCTACGTTGG 1002
QY 302 GCAACTACATTAATGCAATTAACCAAGTTCGCCAAAGACGCTCGCTTATCGGCG 361
DB 1003 AGGACCTCTAGTATGCGCTCACCCAGCTCAAAACCATAGATCAAGCTCGGCA 1062
QY 362 GTATGAGTTGGAACAAACGTTTGAAGACGCAAGCAATCAACAGTACGCTCTCCG 421
DB 1063 AACTCTCTGTGACAAAGTCTTCCGAGAACGGAAGTCCCTGAATGCCAGATTGTGATG 1122
QY 422 CCCTCGATGAAGCGCGCGGCTTGGGTGTGAAGTCTTCGTTACGAATCAAGATT 481
DB 1123 CTATCAACCAAGCTGTGATCTGTGGGTATCCGCTGCTCGTTATGATCAAGATA 1182
QY 482 TGTGTTCCGCGCAAGAAATCTTTCGCGCAATGACGACCAATTAACGCGCAAGCG 538
DB 1183 TCCATGTGCCACCCCGGTGAAGAGTCTATGACAGATGACAGTGGGCGCAAGAGGGT 1242
QY 539 -----AAAAAGCGCGCGTATGTCGCAATCGAAGCGGTAAATCGAACAATCAACC 592
DB 1243 GGGAAAGAGGCTCAGGGCTCAGTGAAGGACAGACGGCGAAACGGCCACAGTTCTAG 1302
QY 593 TTGCAAGTGTCAAGCGTGAAGCCGAATCAACAATCGAAGCGAGCTCAGCTCGG 652
DB 1303 AGTCTGAGGGAGACCGAAGATCGGCAATGTGGCAGAAAGGAAGAAACAGGCCCA 1362
QY 653 TCAATGCGTCCAAATGCGAAGAAATCGCCGATCAACCGCGCAAGGCGAAGCGGAAT 712
DB 1363 TCTCGGCTTCGAAAGCAAGAAAGGCTGAACAGATTAATCAAGCAGCAGAGGCGCA 1422
QY 713 CCCTGCGCTTGTGGCGAAGCAATGCGAAGCATCCGTCAATTGCGCGCGCTTC 772
DB 1423 CAGTTCTGCGCAAGGCTAAGCTTAAGCTTAAGCTTAAGCTTCTGCTGCACTCTGA 1482
QY 773 AAACCCAGAGCGGCGGATCGGTCAATCTGAAGATTGCGAAACAATACGTAACCGGCT 832
DB 1483 CACAACATTAATGAGATGACAGAGTTCACTGAGCTGTGGCGAGAGATATACGCGGT 1542
QY 833 TCAACATCTTGGCCAAAGAAACAAATACGCTGATTTATCCCGCAATTTGCGCATCG 892
DB 1543 TCTCCAAATGCGCCAAAGACTTCCAACTATCTACTGCTTCCAAACCTGCGCATGTCA 1602
QY 893 GCAGCTGATTTTGGCGCGCATG 915
DB 1603 CCAGCATGTGCTCAGGCGCATG 1625
```

RESULT 9

US-10-260-238-266
; Sequence 266, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Krebs, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; PILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 266
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-266

Query Match 16.9%; Score 160.2; DB 17; Length 1218;
Best Local Similarity 53.4%; Pred. No. 4.3e-43;
Matches 336; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

```
QY 60 CGTATCCCCCAGCAGAAAGTCCAGTGTGCGAAGGCTCGGCGTTTCCATGCGCGCT 119
DB 258 CATGCTCCGAGAAAGAGGGTTCGTGTGAGCGGTCGCAAGTACGTCAAGAGCT 317
QY 120 GACGCGCGGTTGAATTTTGAATCCCTTATATGACCGGTCGCGCATTCGGCT 179
DB 318 CGGCTCGGAAATCCAGTGTGCTCGTCCCTCTGTCGACCGCATGCTCACTGCTGCT 377
QY 318 GAAAGAAATCCCTTGAAGCTACCCAGCTGATGCAAGCTCGCTCATACGCAATT 239
DB 378 CAGAGAGAGGCAATCCCAATCCCGACAGTCCGCAATCAACAGAGCAACGCTCAT 437
QY 240 GACTGTGACGCGATCATCTATTTCCAAAGTAAACGATCCCAACTCGCTCATACGTT 299
DB 438 CCAGATCGAGCGCTCTCTACGTCAGATTTGATCCCACTTCTCTATGTGT 497
QY 300 GAGCACTACATTAATGCAATTAACCAAGCTTGGCCAAACGAGTGGTCCGTATCG 359
DB 498 GGAATATCCAAATTTTTCAGTCAATACAGCTTGCCTCAACAACTATGAGAGTGA 557
QY 360 GCGTATGAGTGTGCAAAAAGTTTGAAGAACGCGCAAGAAATCAACGATACGCTCTC 419
DB 558 AAAGATTACGCTTAACAAAGCTTTTGAAGAGAGGATACATTAATAGCAAAATTGTAG 617
QY 420 CGCCTCGATGAAGCCCGCGGCTTGGGTGTGAAGTCTCTCGTTACGAATCAAGGA 479
DB 618 GTCCATTATAGAGCTCACTGATTTGGGAGCTGAATGCTCTCGTTATGAGTCAAGGA 677
QY 480 TTGTTGTTCCGCGCAAGAAATCTTCCGCAATGACAGCACAATTAACGCGCAAGCG 539
DB 678 TATATCTCCGCAAGCTGTGTATTAAGTGTGCTATGAGATCGACAGAGAGGAAAGAA 737
QY 540 AAAAGCGCGCGTATTTGCGCAATCGAAGCGGTAATCGAACAATCAACTTTCAG 599
DB 738 AAAGCGTCCCAAAATCTTGAATGAGAGGTGCTATGTGATGAGGCAAAATCCGCGCAA 797
QY 600 TGTACAGCTGAAGCCGAAATCCAAATCGAAGGCGGCTCAGGCTGCGTCAATGC 659
```

Db 798 GGGTGAAGCTAGAGCAATTTCTTGCAAGCTGAGCAACTGCTGAGGAATTCAGATTGGT 857
Gy 660 GTCCCAATGCCGAGAAATATGCCCGCATCA 688
Db 858 CTCTGAGGCTCATTGAGGACCAAGGCGACGA 886

RESULT 10

US-10-437-963-76664
Sequence 76664, Application US/10437963
Publication No. US2004012343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 76664
LENGTH: 1621
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_76639C.1
US-10-437-963-76664

Query Match 16.9%; Score 160.2; DB 19; Length 1621;
Best Local Similarity 53.4%; Pred. No. 4,9e-43;
Matches 336; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

Gy 60 GGTATCCCGCCGAGCAAGTCCAGTGTGCGAAAGGCTCGGAGCGTTTCATCGCGCCCT 119
Db 258 CATCTGCGCGAGAAAGAGCGTGTGTGAGCGGTTTGGCAAGTACGTAAGACGT 317
Gy 120 GACGCGCGGTTTGAATATTTTGAATCCCTTTATCGACGCGGTGCGCTTACCGCTTCCGT 179
Db 318 GCGGCTCGGAGTCCAGCTGCTGCTCCCTCGTCCGACGCGCTTACGCTTACGCTCGCT 377
Gy 180 GAAAGAAATCCCTTTAGACGTACCGACGAGCTGTGATCAGCGCGATATATAGCAAT 239
Db 378 CAGGAGGAGGCGCATCCCATCCCGACCAATCCCGCATCACCAAGACAAAGCTTCAT 437
Gy 240 GACTGTGAGCGGATCATATTTTCCAAATACCAATCCCAACTGCGCTTACGCTTACGCTTC 299
Db 438 CCAATTCGAGCGGCTCTTACGTCAAGATTTGTATTCCTTACCTTCTTCTTATGTGT 497
Gy 300 GAGCACTCATATATGCAATTAACCAAGCTTGGCCCAAGACGCTGCTTCCGTATCG 359
Db 498 GAGAGATCAATTTTGGATCATACAGCTTGGCCCAACATATGAGAAAGAGCTTGG 557
Gy 360 GCGTATGAGTTGAGCAAAAAGTTGAAGAGCGCAAGAAATCAAGTACGCTGTCTC 419
Db 558 AAGATTAAGCTAGACAAAGCTTTTGAAGAGGAGATACATAAATGACAAATTTGTAG 617
Gy 420 CGCCCTCGAGTAAGCGCGGCGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGGA 479
Db 618 GTTCATTAATAGAGCTGCAATGATTTGGGAGCTGAATGCTTCTCTTATGAGATCAGGA 677
Gy 480 TTTGTTCCGCGCAAGAAATCTTTCGCGCAATGAGGACCAATTAACGCGCAAGCGCA 539
Db 678 TATATCTCGGCAAGCTGTATGAGTGTGCTATGAGATGCAAGCAAGCAAGAAAGAA 737
Gy 540 AAAAGCGCGCTGATTTGCGGAATCCGAAGCGCTAAATCAAGCAATCACTTCCGAG 599

Db 738 AAAGGTGCCCAATTCCTTGATCAGAAAGTGTATGTTGATCAGCAAAATCCGCAAA 797
Gy 600 TGTGAGCTGTAGAGCCCAATTCACATTCGAAAGGCGAGGCTCAGCTCGGCTCAATGC 659
Db 798 GGGTGAAGCTAGAGCAATTTCTTGCAAGCTGAGCAACTGCTGAGGAATTCAGATTGGT 857
Gy 660 GTCCCAATGCCGAGAAATATGCCCGCATCA 688
Db 858 CTCTGAGGCTCATTGAGGACCAAGGCGACGA 886

RESULT 11

US-10-424-599-80498
Sequence 80498, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 80498
LENGTH: 1722
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_43706C.1
US-10-424-599-80498

Query Match 16.8%; Score 158.8; DB 18; Length 1722;
Best Local Similarity 51.1%; Pred. No. 1.5e-42;
Matches 428; Conservative 0; Mismatches 377; Indels 33; Gaps 1;

Gy 65 TCCCCAGAGCAAGTCCAGTGTGCGAAAGGCTTGGGCGTTTCCATCGCGCCGCGCG 124
Db 259 TCCCGAGAGAAAGCGTGTGTGATGAGCGATTCGGGAAGTACGTAAGCTTCCCT 318
Gy 125 CCGGTTGAATTTTGAATCCCTTTATCGACCGGCGTCCATACCGCATTCGCGGAAG 184
Db 319 CCGGAATCAATTTTGAATCCCTTCTGTGATGAGTGTATGATGCTTATGCTCAAG 378
Gy 185 AATCCCTTTAGACGTACCAAGCAAGTCTGATCAGCGCGATATATAGCAATGACTG 244
Db 379 AAGAGCTTATAGCTATCCCGACAGAGCTATACCAAGACATGACCATCATCA 438
Gy 245 TTGACGGATCATATATTTTCAAGTAAACGATCCCAACTGCGCTCATACGTTGAGCA 304
Db 439 TTGACGGGCTCTTATATGCAAGTGTGATCTTAAAGCTGCGCTTATGAGGAGCA 498
Gy 305 ACTATATATGCAATTAACCGAGCTTCCCAAGCAAGCTGCGTTCCTTATCGGCGTA 364
Db 499 ATCCCAATTAATCTGATTAATGCTGCGACAGACAAAGTGTGAGCTTGTATGA 558
Gy 365 TGAAGTTGACAAAGCTTTGAAGAGCGCAAGAAATCAAGTACCGCTCTCCGCC 424
Db 559 TTAATCTTGAAGAGCTTTGAGAAAGGAGACACTCAATGAAGAAATGAGAGTCA 618
Gy 425 TCGATGAAGCCCGCGGCGCTTGGGGTGTGAAGTCTCCGTTACGAATCAAGATTGG 484
Db 619 TTAATATGCTCAAAAAGTTGGGCTTGAAGTCTTGAATGAAGAAAGGATATCT 678
Gy 485 TTCCGCGCAAGAAATCTTCCGCGCAATGCAAGCAATTAACGCGCAAGCGAAAG 544
Db 679 CTCTTCAAGTGAAGAGAGAGCTATGAGATGCAAGACAGAGCAAGAAAGAAAG 738
Gy 545 GCGCCGTAATGCGCAATCCGAAGCCGTAATCAAGCAATCACTTGGCCAGTGTCT 604
Db 739 GAGCTTAATTTCTTATGCTGAAGAGAAAGCAGCTCAATTAACATTTGCTGATGAA 798

ORGANISM: Homo sapiens
US-10-956-157-7085

Query Match 16.4%; Score 155.6; DB 21; Length 1303;

Best Local Similarity 50.6%; Pred. No. 1.6e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

```
QY TCATCCCCCAGAGAGATCCAGTGTGCGAAAGGCTCGGGCGTTTCCATCGCCCTCGA 121
DB TCGTCCCGCAGAGAGGCTGGGTGGTGGAGCGAATGGCGATTCCACCGGATCTCG 241
QY 122 CGGCGGTTTGAAATTTTGAATTCCTTATCGACCGCGTGCCTTACCGCATTCGCTGA 181
DB 242 AGCTGGTTGAACATCTCATCTCTGTGTAGACCGATCCGATATGTGAGAGTCTCA 301
QY 182 AAGAAATCCCTTATAGACCTACCCAGCAGTCTGATCAACCGCGATATATGCGAATGA 241
DB 302 AGGAAATGTGATCAACGTCGCTGAGCAGTGGCTGTGACTCTGCAATGTAACTCTGC 361
QY 242 CTGTTGACGGCATCTATTTCAGATTAACCGATCCCAACTCGCTCATACGGTTCGA 301
DB 362 AATGATGAGATCTTTTACCTGGCATCATGAGACCTTACAGGCAAGCTACGGTGG 421
QY 302 GCAACTACATTATGCAATTACCCAGCTTGCCTCAAGACGCTGCTTTCGTTATCGGAC 361
DB 422 AGGACCTGAGTATGCGTCAACCGAGCTCAAAACATGATGATCAAGAGCTCGGCA 481
QY 362 GTATGAGATTTGAGCAAAACGTTTGAAGAACGCAAGAAATCAACGATACCGTCTCG 421
DB 482 AACTCTCTGTGACAAAGTCTTCCGGAAAGGAGTCCCTGAATGCCAGATTTGGATG 541
QY 422 CCTCTGATGAAGCCCGCGGCTTGGGGTGTGAAGTCTCTCGTTACGAAATCAAGAT 481
DB 542 CCATCAACCAAGCTGCTGATCTGGGGTATCCGCTGCTCTGTTATGATGATCAAGATA 601
QY 482 TGGTTCCGCGCAAGAAATCTTGGCGATGCAAGCAAAATTAACCGCGAAGCGGAAA 541
DB 602 TCCATGTGCAACCCCGGGTGAAGAGTCTATGCAATGCAAGTGAAGGCAAGCGCGCA 661
QY 542 AACCGCGCCGATTTGCCGAATCCGAAGGCCGTAATGAAACAAATCAACCTTGCATG 601
DB 662 AACGGGCCACAGTTCTGAGTCTGA-----GG 688
QY 602 GTACAGCTGAAGCCGAAATCCAAACATCCGAAGCGAGGCTCAAGCTCGGTCATGCGT 661
DB 689 GGACCCGAGAGTGGGCAATCAATGCGAAGAGGAAAGAAACAGGCCCAAGATCTGGGCT 748
QY 662 CCAATGCCGAGAAATGCGCCGCAATCAACGCGCGCAAGCGAAGCGGAATCCCTGCGCC 721
DB 749 CCGAAGCAGAAAGGCTGAACGATTAATCAAGGCAAGAGAGGCAAGTCAAGTCTGCG 808
QY 722 TTGTTTCCGGAAGCCATGCCAAGCATCCGTCAAATTTGCCCGCCCTTCAACCCGAG 781
DB 809 CGAAGGCCAAGGCTTAAGCTGAAGTATTTGAATCTGCTGCAAGCTTGAACAACATTA 868
QY 782 GCGGGCGGATGCGGTCATCTGAAGATTGCGGAACAATAAGTACGCGCTTCAACAATC 841
DB 869 ATGAGATGCAAGCACTTCACTGAGTGGCCGAGCAATATGTCAAGCCGCTTCTCAAC 928
QY 842 TTGCGAAGAAAGCAATACGCTGATTTATCCCGCAATGTTGCCGATCGGAGCTCGA 901
DB 929 TGGCCCAAGAGCTCCAACTATCTATGCTTCAACCTTGGCGATGTCAACAGCATGG 988
QY 902 TTTTTCGCGGCAATG 915
DB 989 TGGCTCAGGCGCATG 1002
```

RESULT 16
US-10-276-774-1001/c
; Sequence 1001, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:

```
APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 1001  
; LENGTH: 1398  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-1001
```

Query Match 16.4%; Score 155.6; DB 18; Length 1398;
Best Local Similarity 50.6%; Pred. No. 1.7e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

```
QY 62 TCATCCCCCAGAGAGATCCAGTGTGCGAAAGGCTCGGGCGTTTCCATCGCCCTCGA 121
DB 1212 TCGTCCCGCAGAGAGGCTGGGTGGTGGAGCGAATGGCGGATTCACCGATCTCG 1153
QY 122 CGGCGGTTTGAAATTTTGAATTCCTTATCGACCGCGTGCCTTACCGCATTCGCTGA 181
DB 1152 AGCTGGTTGAAATCTCTATCTCTGTGTAGACCGATCCGATATGTGAGAGTCTCA 1093
QY 182 AAGAAATCCCTTATAGAGTACCCAGCCAGCGTCTGATCAACCGCGATTAAGCAATTGA 241
DB 1092 AGGAAATGTGATCAACGTCGCTGAGCAGTGGCTGTGACTCTGCAATGTAACTCTGC 1033
QY 242 CTGTTGACGGATATCTATTTCAGATTAACCGATCCCAACTGCGCTTCAACGTTTGA 301
DB 1032 AATGATGAGTCTTTTACCTGGCATGAGACCTTTCAGAGCAAGCTACGGTGG 973
QY 302 GCAACTACATTATGAGCAATTAACCGCTTGCCTCAAGACGAGCTCGTTCCGTTATCGGAC 361
DB 972 AGGACCTGAGTATGCGCTGACCCAGCTAGCTCAAAACATGATGATCAAGAGCTCGGCA 913
QY 362 GTATGAGTTGGACAAAACGTTTGAAGAACGCAAGAAATCAACGATACGTCGTTCCG 421
DB 912 AACTCTCTGTGACAAAGTCTTCCGGGAAACGGAGTCCCTGAATGCCAGCATTTGATG 853
QY 422 CCTCTGATGAAGCCCGCGGCTTGGGCTGTGAAGTCTCTCCGTTTGAATCAAGATT 481
DB 852 CCATCAACCAAGCTGCTGATCTGGGGTATCCGCTGCTCTCGTTATGATCAAGATA 793
QY 482 TGGTTCCGCGCAAGAAATCCTTGGCGAATGACAGGCAAAATTAACGCGCGAAGCGGAAA 541
DB 792 TCCATGTGCAACCCCGGGTGAAGAGTCTATGCAATGCAAGTGAAGGCAAGAGCGGGA 733
QY 542 AACCGCCCGATTTGCCGAATCCGAAGCCGTAATGAAACAAATCAACCTTCCAGTG 601
DB 732 AACGGGCCACAGTTCTGAGTCTGA-----GG 706
QY 602 GTACAGCTGAAGCCGAAATCCAAACATCCGAAGCGAGGCTCAAGCTGCGTCAATGCGT 661
DB 602 GTACAGCTGAAGCCGAAATCCAAACATCCGAAGCGAGGCTCAAGCTGCGTCAATGCGT 661
QY 705 GGAACCGAGAGTTCGCGCATCAATGTGCGAAGAGGAAAGAAACAGGCCCAAGTCTGGGCT 646
DB 662 CCAATGCCGAGAAATGCGCCGCAATCAACGCGCGCAAGCGGAAGCGGAATCCCTGCGCC 721
QY 645 CCGAAGCAGAAAGGCTGAACAGTAAATCAAGGACAGAGAGGCCAAGTCAATTTCTGG 586
DB 722 TTGTTCCGGAAGCCATGCGAAGCCATCCGTCAAATTTGCCCGCCCTTCAAAACCAAG 781
QY 585 CGAAGGCCAAGGCTTAAGGCTGAAGCTATTTGAATCTGCTGCACTGTGACAAACATA 526
DB 782 GCGGGCGGATGCGGTCATCTGAAGATTGCGGAACAATAAGTACGCGCTTCAACAATC 841
QY 525 ATGAGATGCAAGCTTCACTGAGTGGCCGAGAGTATGTGAGGCGCTTCTCAAC 466
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QY 842 TTGCCAAGAAAGCAATACGCTGATTATGCCCCCAATGTTCCGACATCGGACGCTTGA 901
DB 465 TGGCCAAAGACTTCACAACTATCTACTGCTCCAAACCCCTGGCATGTGCACAGCATGG 406
QY 902 TTTCTGCGCGCATG 915
DB 405 TGGCTCAGGCGCATG 392

RESULT 17
US-10-357-930-24973

; Sequence 24973, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24973
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: 1841..1842
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-24973

Query Match 16.4%; Score 155.6; DB 20; Length 1842;
Best Local Similarity 50.6%; Pred. No. 1.9e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCGACAGAGATCCAGTGTGCGGAGCTCGGCGGTTTCATCCGCGCCCTGA 121
DB 661 TGTGCGCGACAGAGCGCGCTGTGTGAGAGCAATGCGCGCATTCACCGCATCTGG 720
QY 122 CGGCGGTTTGAATATTTGATTCCTTTATGACCGCGCTGCGCTACCGCATTTGCTGA 181
DB 721 ACCCTGTGTTGAACATCTCATCTCGTGTGTTAGACCGGATCCGATATGTGCGAGTCTCA 780
QY 182 AAGAAATCCCTTGAAGTACCGACGAGTGTGATTCACGCGCGATTAATACGCAATTGA 241
DB 781 AGGAATTTGTCAACAGTGTGCGCGAGTGTGATCTCGACAAATGTAACTCTCG 840
QY 242 CTGTGACGCGCATCTATTTTCAAGTAAACGATTCGAACTCGCTCATACGTTTGA 301
DB 841 AATCATGATGAGTCTTTACTGCGCATATGAGACCTTAAACAGGCAAGCTACGCTGTG 900
QY 302 GCAACTACATTAATGCAATTAACCGACTTGGCCCAAGAGCGGTGCGTTATGCGGG 361
DB 901 AGGACCTGATGTGCGCTGATCCAGCACTAGCTCAAAACATGATGAGAGCTGGCA 960

QY 362 GTATGAGTGTGACAAAGCTTTGAAGACGAGCAAAATCAACAGTACCGTCTCCG 421
DB 961 AACTCTCTGTGACAAATCTTTCGGGAACGAGATCCCTGATATCCAGCATTTGATG 1020
QY 422 CCTGTGATGAAGCGCGCGGCTTGGGCTGTGAAGTCTCTCGTTACAAATCAAGATT 481
DB 1021 CCATCAACCAAGCTGTACTGTGCGGTATCCGCTGCTCGTTATGATCAAGATTA 1080
QY 482 TGTTCGCGCGCAAGAAATCTTGGCGCATATGACGACCAATTAACCGCCGAACCGAAA 541
DB 1081 TCCATGTCCACCCCGGTGAAGAGTCTATGCAATGAGTGAAGGACGAGCGCGGA 1140
QY 542 AACGCGCCCGTATTGCGCAATCCGAAGGCGGTAAATGAAACAATCAACCTGCGAGT 601
DB 1141 AACGGGCGACAGTTCTTAAGTCTGA-----GG 1167
QY 602 GTACGCTGTGAAGCGCAATTCACAAATCCGAAGGCGAGGCTCAGGCTCGTCAATGAGT 661
DB 1168 GGAACCGGAGATGCGGCATCTAATGTGCGAAGGAGAAAGAACGCGCATCTGGCT 1227
QY 662 CCAATGCGGAGAAATGCGCCGATCAACCGCGCAAGGCGAAGCGGAATCTGCGCC 721
DB 1228 CCGAAGCAAGAAAGGCTGAACAGATTAATCAGGCGAGAGAGCCAGTGCAGTTCTTG 1287
QY 722 TTGTTGCGGAGCCCAATGCGCAATCCGTCAAATTGCGCGCCCTTCAAAACCAAG 781
DB 1288 CGAAGCGCAAGCTTAACCTGAAGTATTCGAATCTGCTGACCTCTGACACAACTA 1347
QY 782 GCGGGCGGATGCGGTCAATCTGAATTTGCGGAACAATACGTACCGGTTCACAAATC 841
DB 1348 ATGAGATGACAGACTTCACTGACTGTGCGGACAGATATGTCAAGCGGTTCTCAAC 1407
QY 842 TTGCCAAGAAAGCAATACGCTGATTATGCCCCCAATGTTGCCAATGCGAGCTTGA 901
DB 1408 TGGCCAAAGACTCCAACTATCTACTGCTCCCAACCTGCGCATGTCAACAGATGG 1467
QY 902 TTTCTGCGCGCATG 915
DB 1468 TGGCTCAGGCGCATG 1481

RESULT 18

US-10-198-846-12975
; Sequence 12975, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12975
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: 1..2, 1909, 1910
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-12975

Query Match 16.4%; Score 155.6; DB 14; Length 1910;
Best Local Similarity 50.6%; Pred. No. 2e-41;

Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY TCATCCCCCAGAGAGATTCACCGTTGCGAAGGCTGGGGGTTTCATGCGCCCTGA 121
Db TCGTCCCGCAGAGAGAGCTGGGTGGAGCCGATGGCCGATTCACCGGATCTGG 241
QY 122 CGGCGGTTTGAATATTTGATTCCTTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
Db AGCCGGTTTGAATCTCTCATCCCTGTGTAGACCGGATCGAATATGAGAGATCTCA 301
QY 182 AAGAAATCCCTTTAGAGCTACCGACCGGTCTGATCACCGCGCATTAATACGAATGA 241
Db AGGAAATGTCAATCAACGTGCTGAGCGGTGATCTGATCTGCAATATTAATCTGTC 361
QY 242 CTGTGAGCGGATCATCTATTTCGAAGTACCGATCCCAACTGGCTCATACGGTTGCA 301
Db 362 AAATGATGAGTCTTTTACTGCGCATCATGACCTTTACAGGCAAGCTACGGTGG 421
QY 302 GCAACTACATTATGCAATTAACCGCTTGGCCCAACGACGCTGGCTTCCGTTATCGGGC 361
Db 422 AGGACCTGAGTATGCGGTACCGCTGAGCTCAAGCTCAAAACATGATCAAGGCTCGCA 481
QY 362 GTATGAGTGTGACAAAACGTTTGAAGAAGCGACGAATCAACATTCCTGCTTCG 421
Db 482 AACTCTCTGTGACAAAGTCTTCCGGGAAAGGAGTCCCTGAATGCGCATTTGGATG 541
QY 422 CCTCTGATGAAGCGCGGGGCTTGGGGTGAAGTCTCCGTTACGAATTCAGATTA 481
Db 542 CCAATACCAAGCTGTACTGCTGGGTATCCGCTGCTCGTTATAGATCAAGATTA 601
QY 482 TGGTTCCGCGCAAGAAATCTTTCGCGAATGACGACCAAAATTAACCGCGCAACGCGAA 541
Db 602 TCATATGTCACCCCGGGTGAAGAAGTCTATGAGATGAGATGAGGAGGAGCGGGCGA 661
QY 542 AACGCGCCCGTATGTCGCAATCCGAGGCGCTAAATGAAACAATCAACCTTGCAGTG 601
Db 662 AACGCGCCACAGTCTTGAAGTCTGA-----GG 688
QY 602 GTACGCGTGAAGCGCAATTCGAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCGT 661
Db 688 GGACCCGAGAGTCCGCTCATATGAGGAGAGGAGAGAAACAGGCCCAAGTCTGAGCT 748
QY 662 CCAATGCGAGAAATTCGCCCGCATCAACGCGCGAAAGCGAAGCGGAATCCCTGCGCC 721
Db 749 CCGAAGCGAGAAAGGCTGAACAGATTAATCAAGGACGAGAGAGGCGAGTCAAGTTCG 808
QY 722 TTGTTGCGGAGGCAATGCGCAAGCTCGTCAATTCGCGCGCTTCAAAACCGCAG 781
Db 809 CGAAGGCGAAGGCTTAAGCTGAAGCTATTCGAATCTGGCTGCAAGCTCTGACACAACTA 868
QY 782 GCGGGGCGGATGCGGTCAATCTGAAGATTTGCGGAACATATAGCTAGCGGTTCAACATC 841
Db 869 ATGAGATGACAGGCTTCACTGATGTGGCGAGCATATGTCAGCGGTTCTCCAAAC 928
QY 842 TTGCGAAGAAAGCAATACGCTGATTAATCCGCGCAATGTTGCCGACATCGCAGCTGA 901
Db 929 TGGCGCAAGAGCTCCAAACTATCTCACTGCTCCCAACCTGGGAGATTCACAGCATGG 988
QY 902 TTTCTGCGCGCATG 915
Db 989 TGGCTCAGGCGCATG 1002

RESULT 19

US-10-119-428-37
; Sequence 37, Application US/10119428
; Publication No. US2003016581A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Wehrman, Tom

APPLICANT: Ren, Feiyan
APPLICANT: Ma, Yunding
APPLICANT: Zhou, Ping
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Drmanac, Radje T.
TITLE OF INVENTION: No. US2003016581A1el Nucleic Acids and
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,428
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: pl_fl_genes Version 1.0
SEQ ID NO 37
LENGTH: 9098
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (75) .. (9098)
US-10-119-428-37

Query Match 16.4%; Score 155.6; DB 16; Length 9098;
Best Local Similarity 50.6%; Pred. No. 4.4e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

QY 62 TCATCCCCCAGAGAGATTCACCGTTGCGAAGGCTGGGGGTTTCATGCGCCCTGA 121
Db 193 TCGTCCCGCAGAGAGAGCTGGGTGGAGCCGATGGCCGATTCACCGGATCTGG 252
QY 122 CGGCGGTTTGAATATTTGATTCCTTTATCGACCGCGTGGCTTACCGCATTCGCTGA 181
Db 253 AGCCGGTTTGAATCTCTCATCCCTGTGTAGACCGGATCGAATATGAGAGATCTCA 312
QY 182 AAGAAATCCCTTTAGAGCTACCGACCGAGTGTGATCACCGCGATTAATACGAATGA 241
Db 313 AGGAAATGTCAATCAAGTGTGAGAGTGGCTGTGACTCTGACCAATGTAATCTGTC 372
QY 242 CTGTGAGCGGATCATCTATTTCGAATTAACCGATCCCAACTGCGCTCATACGGTTTGA 301
Db 373 AAATGATGAGTCTTTTACTGCGCATCATGACCTTTACAGGCAAGCTACGGTGG 432
QY 302 GCAACTACATTATGCAATTAACCGAGCTTGGCCCAACGACGCTGCTTATCGGGC 361
Db 433 AGGACCTGAGTATGCGGTCAACCGAGCTAGCTCAAAACCATGATGATCAGAGCTCGCA 492
QY 362 GTATGAGTGTGACAAAACGTTTGAAGAAGCGGACGAATTAACAGTACCTGCTTCG 421
Db 493 AACTCTCTGTGACAAAGTCTTCCGGAGCGGAGGCTCTGAATGCCAGCATTTGTGATG 552
QY 422 CCTCGATGAAGCGCGGGCTTGGGGTGAAGTCTTCGTTAGAAATCAAGATT 481
Db 553 CCAATCAACAGAGCTGTGATGCTGGGGTATCCGCTGCTGTTATGAGATCAAGATA 612
QY 482 TGGTTCCGCGCAAGAAATCTTTCGCGCAATGACGAGCAAAATTAACGCGCAAGCGAAA 541
Db 613 TCATATGTCACCCCGGGTGAAGAAGTCTATGAGATGAGATGAGAGGAGCGGCGA 672
QY 542 AACGCGCCCGTATGTCGGAATCCGAGGCGGTAAATCGAACAATCAACCTTGCAGTG 601
Db 673 AACGCGCCACAGTCTTGAAGTCTGA-----GG 699
QY 602 GTACGCGTGAAGCGGAATCCGAATCCGAAGCGAGGCTCAGGCTGCGGTCAATGCGT 661
Db 700 GGACCCGAGAGTCCGCTCATATGTCGAGAGAGAGAGAAACAGGCCCAAGTCTTGGCT 759
QY 662 CCAATGCGGAGAAATGCGCGCATCAACGCGCGCAAGGAGGAGGAGATCCCTGCGCC 721

Accession	Sequence	Position
Db	CGAAGCCAGAAAGGCTGACAGATTAATCAGCAGACGAGAGGCCAGTGCAGTTCTGG	81.9
Oy	TTGTTGCCGAAACCATATGCCGAGCCATCCGTCAAAATGGCCGCGCCCTTCAAAACCCAG	78.1
Db	CGAAGCCAGAGCTGAAGCTGAAGCTGATTCGATCCTGGCTGCAGCTCTGCACACAACTA	87.9
Oy	GCGGGGCGGATCCGGTCACTATGGAATGGCGGAAACAATACGTAGCCGCGCTTCAACATC	84.1
Db	ATGGAGATGACGACAGCTTCACTGACTGCTGTGGCCGACGATATGTCAAGGCGCTTCCAAAC	93.9
Oy	TTGCCAAGAAGCAATACGCTGATATATCCCGGCCCAATGTGGCGCATGGGAGCGCTGA	90.1
Db	TGGCCAAAGGATCCCAACACTATCTACTGCTCTCAACCTGGCGATGTCAACGACATGG	99.9
Oy	TTTCTGCCGCGCATG	91.5
Db	TGGCTCAGGCCATG	101.3

```

RESULT 20
US-10-291-172-34
; Sequence 34, Application US/10291172
; Publication NO. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/566,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 34
; LENGTH: 9098
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (75)..(9095)
US-10-291-172-34

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Query Match	16.4%;	Score 155.6;	DB 17;	length 9098;
Best Local Similarity	50.6%;	Pred. No. 4,4e-41;		
Matches 432; Conservative	0;	Mismatches 389;	Indels 33;	Gaps 1

QY 62 TCAATCCCCACGACGAGAAAGTCACAGTGTGTGAAAGAGCTGGGGGCTTTCATTCGGGCCCTGA 121

Db 193 TGTGTCCCGACGACGAGGAGGCGCTGGTGTGTGAGCGAAATGGGCGCATTCACCCGAAATCTCTGG 252

OY 122 CGAGCCGGTTTGAATATTTTGAATTTCCCTTTATCGACCGCGTGCCTACCGGCATTCGCTGA 181

Db 253 AACCTGGTTTGAACATCTCTCATCTCCGTGTGTGAACCGAATTCGATATGTGCAAGCTCTGA 312

OY 182 AAGAAATCCCTTTAGACGTACCCGACGAGCTGTGCATCACGCGCGATTAATAGCAATTGA 241

Db 313 ACGAAATTTTCATCAACGTGCTGACGACAGTCGGCTGTGACTTCGACAAATGTAACCTGCG 372

OY 242 CTGTTGACGCGCATCATCTATTTTCCAGTAACCGATCCCAAACTCGGCTCTAATACGTTTCCA 301

Db 373 AAATCGATGAGTCTCTTAACTGCGCATCTGAGACCTTAAAGGCAAGCTAAGGTGTGG 432

OY 302 GCAACTACATTATGGCAATTACCGACGCTGGCCAAACGACGTGCTTCCGTTATTCGGGC 361

Db 433 AGGACCCCTGAGTATGCCGTCACCCAGCTTAGCTCAACACATGAGATCAGAGCTCGGCA 492

Qy 362 GTATGAGATTGACAAACGTTTGAAAGACGCGACGAAATCAACAGTACCCTGCTCCG 421

Db 493 AACCTCTCTCGGACAAAGCTCTCCGGGAAACGGAGATCCTCGAATGCAACATTTGTGATG 552

Qy 422 CCCCTGATGAAAGCCGCGGGGCTTGGGGGTGAAAGTCCCTCGGTTACGAATCAAGATT 481

Db 553 CCATACACCAAGCTCTGACTGCTGGGGTATCCGCTGCTCCGTTATGAGATCAAGATA 612

Qy 482 TGGTTCCGCCCGCAGAAATCCTTCGCGCAATGCAAGGCACAAAATTACGCCGGAACGCGAAA 541

Db 613 TCATATGTCACACCCGGGGAAAGAGTCTATGACATGCAGGTGAGAGGACAGCCGCGGA 672

Qy 542 AACCGGCCCGATTATGCCCAATCCGAAAGGCCGTAAATCGAACAAATCAACCTTGCCAGTG 601

Db 673 AACGGGGCCACAGTTCTAAGTCTGA-----GG 699

Qy 602 GTACACGTGAAGCCGAAATCCAAACAATCCGAAGCGAGGCTCAGGCTCGGTCATGCGT 661

Db 700 GGACCCGAGAGTCGCGCATCATATGTGGCAGAAAGGAAAGAAACGCGCCAGATCTGGCCCT 759

Qy 662 CCAAATGCCGAAGAAATTCGCCGCCATCAACCGCGGCCAAAGGCGAAGGGAATCCCTGCGCC 721

Db 760 CCGAAGCGAAGAAAGGCTGAAACAGTAAATCAAGGACGACGAGAGGCGCAGTGCAGTTCTGG 819

Qy 722 TTGTTGCCGAAGCCAAATGCGCGGCAATCCGTCMAATTGCGCGCGCCCTTCAAAACCCAG 781

Db 820 CGAAGGCCAAGGCTAAAGCTGAAGCTATTGCAATCTGGCTGACGCTGACACCAACATA 879

Qy 782 GCGGGGCGGATCCGCTCAATTTGAAGATTGCGGAACAATACGTAGGCGGCTTCAACAATC 841

Db 880 ATGAGAGATGCACACACTTCACTGACTGTGCGCGAGCAGTATGTCAAGCGCCTTCCAAAC 939

Qy 842 TTGCGAAGAAAGCAATACGTGATTATGCTCCGCGCATGTTCGCGCATTCGAGCGCTGA 901

Db 940 TGGCCAAAGCACTCAACACTATCTACTGCTCCCTCCAAACCTGGCGATGTCAACAGCATGG 999

Qy 902 TTCTTCGCGCGCATG 915

Db 1000 TGGCTTCAGGCGCATG 1013

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/ RESULT 21
/ US-10-221-278-34
/ Sequence 34, Application US/10221278
/ Publication No. US20040034208A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: No. US20040034208A1 Nuclear Acids and Polypeptides
/ FILE REFERENCE: 21272-045
/ CURRENT APPLICATION NUMBER: US/10/221,278
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: 09/593,267
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 09/665,363
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 09/616,847
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 09/596,193
/ PRIOR FILING DATE: 2000-06-17
/ PRIOR APPLICATION NUMBER: 09/544,454
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: 09/519,705
/ PRIOR FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 752
/ SEQ ID NO 34
/ LENGTH: 9098
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/

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LOCATION: (75) .. (9095)
US-10-221-278-34

Query Match 16.4%; Score 155.6; DB 18; Length 9098;

Best Local Similarity 50.6%; Pred. No. 4.4e-41;
Matches 432; Conservative 0; Mismatches 389; Indels 33; Gaps 1;

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OY 62 TCATCCCCCAGAGAAAGTCAAGTGTGCAAGAGCTGGGGCTTTCCATGCGCCCTGA 121
DB 193 TCGTCCCGCAGAGAGAGCTGGGTGTGAGCAATGGCCGAAATTCACCGGATCTCG 252
OY 122 CGGCGGTTTGAATTTTGAATCCCTTTATGACCGCGTGCCTACCGCATTCCTGA 181
DB 253 AGCGTGTGTAACATCTCACTCCCTGTGTAGACCGATCGAATATGTGAGAGTCTCA 312
OY 182 AAGAAATCCCTTTAGACGTAACCCAGCCAGTGTGATCAACGGCGATATAGCAATGA 241
DB 313 AGGAAATGTCACTCAACGTGCTGAGCAGTGGCTGTGATCTGTGACAAATGTAACCTGC 372
OY 242 CTGTGACGGCATCATCTATTTCNAAGTAACGATCCCAACTCGCTCATATAGGTTTGA 301
DB 373 AAATGATGAGTCTTACTTACCTGGCCATCATGSAACCTTACAGGCAAGCTAACGTTGG 432
OY 302 GCAACTACATTATGSCAATTACCCAGCTTGCCCAACGACGCTGCTTCCTTATCGGCG 361
DB 433 AGGACCTGAGTATGCCGTCAACCCAGCTAGCTCAAAACCATGAGATCAGAGCTCGCA 492
OY 362 GTATGAGTATGAGCAAAAGCTTTGAAGAAAGCGAAGTCAACAGTACCGTCTCG 421
DB 493 AACTCTCTGTGACAAAGTCTTCGGGAAAGGAGTCCCTGAAATGCCAGCATGTGGATG 552
OY 422 CCTCTGATGAAGCCCGGGCTTGGGGTGTGAAGTCTCTCGTTACGAAATCAAGATT 481
DB 553 CCATTAACCAAGCTGTACTGTGGGTATCCCGTGTCTCGTTATGATCAAGATTA 612
OY 482 TGGTTCCGCGAGAAATCTTCCGCGATGCAAGGCAAAATTAACGCCCAAGCGGAA 541
DB 613 TCCATGTGCAACCCCGGGTGAAGAGTATGCAAGTCAAGTGGAGGCAAGCGCGGA 672
OY 542 AACCGGCCGATGTCGGAATCCGAAAGCCGTAATGAAACAATCAACCTTGCAGTG 601
DB 673 AACGGGCCAGTCTGAGTCTGA-----GG 699
OY 602 GTACGCTGAAGCCGAAATCCAAACATCCGAAGCGAGCTGAGCTGCGTCAATGCGT 661
DB 700 GGAACCCGAGAGTCTGGCCATCAATGTGGAGAAAGGAAACAGGCCCAAGTCTCGGCT 759
OY 662 CCAATGCGGAGAAATGCGCCGCAATCAACCGCGCAAGCGAGCGGAATCCCTGCGCC 721
DB 760 CCGAAGCAGAAAGGCTGAACAGATTAATCAGGCGAGAGAGGCCAGTGCAGTTCTGG 819
OY 722 TTGTTGCGAAGCCAAATGCCAGCATCCGTAATTGCGCGCCCTTCAAAACCCAG 781
DB 820 CGAAGGCCAAGGCTTAAGCTGAAGTATTCGAATCTGCTGCAAGCTTGAACAATTA 879
OY 782 GCGGGCGGAGTCCGCTCAATCTGAAGATGCGGAAACAATAGTAGCCGCTTCAACATC 841
DB 880 ATGAGATGCAAGCACTTCACTGACTGTGGCCGAGACATATGTCAAGCGGTTTCTCAAC 939
OY 842 TTGCGAAGAAAGCAATAGCTGATTATGCCGCAATGTTGCGGACATGCGAGCTTGA 901
DB 940 TGGCGCAAGAGCTCCAACTATCTCACTGCTCCAAACCTGCGAGATGTCAACAGCATGG 999
OY 902 TTTCTGCGCGCATG 915
DB 1000 TGGCTCAGGCGCATG 1013
```

RESULT 22

US-09-898-216-2

Sequence 2, Application US/09898216

Patent No. US20020169308A1

GENERAL INFORMATION:

```
APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,216
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,562
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0181 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-898-216-2
Query Match 16.4%; Score 155.2; DB 9; Length 1188;
Best Local Similarity 50.5%; Pred. No. 2.1e-41;
Matches 431; Conservative 0; Mismatches 390; Indels 33; Gaps 1;
```

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OY 62 TCATCCCCCAGAGAAAGTCAAGTGTGCAAGAGCTGGGGCTTTCCATGCGCCCTGA 121
DB 182 TCGTCCCGCAGAGAGAGCTGGGTGTGAGCAATGGCCGAAATTCACCGGATCTCG 241
OY 122 CGGCGGTTTGAATTTTGAATCCCTTTATGACCGCGTGCCTACCGCATTCCTGA 181
DB 242 AGCTGTGTAACATCTCACTCCCTGTGTAGACCGATCGAATATGTGAGAGTCTCA 301
OY 182 AAGAAATCCCTTTAGACGTAACCCAGCTGTCATCAACGGCGATATAGCAATGA 241
DB 302 AGGAAATGTGATCAAGTGTGCTGAGCAGTGGCTGTGACTGTGACAAATGTAACCTGC 361
OY 242 CTGTGACGGCATCATCTATTTCNAAGTAACGATCCCAACTCGCTCATATAGGTTTGA 301
DB 362 AAATGATGAGTCTTACTGCTGCAATGACCTTCAAGGCAAGCTACGTTGG 421
OY 302 GCAACTACATTATGSCAATTACCCAGCTTGCCCAACGAGCTGCTTCCGTTATCGGCG 361
DB 422 AGGACCTGAGTATGCCGTCAACCCAGCTAGCTCAAAACCATGAGATCAGAGTCTCGCA 481
OY 362 GTATGAGTGAAGCAAAAGCTTTGAAGAAAGCGAGCAAGTAACAGTACGTCGTCG 421
DB 482 AACTCTCTGTGACAAAGTCTTCGGGAAAGGAGTCCCTGAATGCAAGCATTTGGATG 541
OY 422 CCTGTGAGAGCGCGGGGCTTGGGGTGTGAAGTCTTCGTTACGAATCAAGATT 481
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DB 5412 CCATCAACCAAGCTCTGACTGCTGGGATATCCGCTGCTGCTTATGATCAAGATTA 601
QY 482 TGGTTCGCGCCGCAAGAAATCTTTCGCGCAATGACGACAAATTAACCGCCGCAAG 541
DB 602 TCATGTCGCAACCCCGGGTGAAGAGTCTATGCAATGCAAGTGAAGGACGCGCGGA 661
QY 5412 AACGCGCCGATTTGCCAATCCGAAAGCCGCTAAATGCAACAATCAACCTTGCAGTG 601
DB 662 AACGGGCCCAAGCTTGAAGTCTGA-----GG 688
QY 602 GTACAGCTGAAGCCCAAAATCCAATCCGAAGCGAGGCTGAGCTGCGTCAATGCGT 661
DB 689 GGAACCCGAGAGTCTGCGCATTAATGTGCGCAAGAGGAAGAAACAGGCCAGATCTGCGCT 748
QY 662 CCAATGCGGAGAAAATCGCCCGCATCAACCGCGCAAGCGAAGCGAATCTTGCCTG 721
DB 749 CCGAAGCAAGAAAAGGCTGAACAGATTAATCAGGCAAGCAAGAGGCAATGCAATCTTG 808
QY 722 TTGTTGCGGAGCAATGCGCAAGCATCCGTCAAATTTGCCCGCCCTTCAACCCGAG 781
DB 809 CGAAGGCCAAGGCTTAAGCTGAAGCTAATTCGAACTCTGCTCAGCTTGAACAACATA 868
QY 782 GCGGGGCGGATGCGGCTCAATCTGAAGATTGCGGAAACATACGTAAGCCGCTTCAACATC 841
DB 869 ATGAGATGCAAGCATTTCACTGACTGTGCGCGAGAGATATGTCAGCGCTTCTCAAC 928
QY 842 TTGCGCAAGAAAGCAATACGCTGATTTATCCCGCCCAATGTTGCCGATCGGACGCTGA 901
DB 928 TGGCCAGAGACTTCAACATTAATCTTCTGCTGCAACCTGCGATGTCACACAGATG 988
QY 902 TTTCTGCGCGCATG 915
DB 989 TGGCTCAGGCGCATG 1002

RESULT 23

US-10-297-465A-1/c
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setudal, Joao
; APPLICANT: Mediane, Joao
; APPLICANT: Arruda, Paulo
; TITLE OF INVENTION: Isolated Genome of *Xylella fastidiosa* and Uses Thereof
; FILE REFERENCE: PAPER 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: *Xylella fastidiosa*
US-10-297-465A-1

Query Match 15.8%; Score 149.8; DB 19; Length 2731748;
Best Local Similarity 51.6%; Pred. No. 7.8e-38;
Matches 343; Conservative 0; Mismatches 322; Indels 0; Gaps 0;
QY 4 GAATTTTCTATATCTTTGTCGACGCGCTGCTTTGCGCTTCAATCTTTGTCGTC 63
DB 195321 GATATTGCGCTCTATTGCTGCTGCGCGGCTCATCTGTTATCAAAATCGCATCATG 195262
QY 64 ATCCCGCAGCAGAGATGCAAGTGTGCAAGAGGCTGCGGCGTTTCAATCGCGCCGTCAGC 123
DB 195261 GTGCCGCAAGGTTATGAGTGCAGCCGTAGAGAAATTCGGTCTTACACCGACACATGAAA 195202

QY 124 GCCGTTTGAATATTTGATTCCTTTATCGAACCGGTCGCTTACCGCATTCGCTGAAA 183
DB 195201 CCGGCTTCATTTCTTATTCCTTTATCGAGCGTGGAGCGCAAGTGAAGATGAG 195142
QY 184 GAATTCCTTTAGACGTACCAAGCCAGGCTTGCATCAAGCGGATTAATGCAATTTGACT 243
DB 195141 GAAACAGTACTGCGTGTACCGGATCAAGAGGTCATCAACAAAGATTAAGCGCGGAGTACGC 195082
QY 244 GTTACGCGCATCATATTTTCCAGTAACCGATCCCAACTGCGCTCATAGGTTGAGC 303
DB 195081 GTAGCGGGGAGTATTTTTCAGGTGCTTCAAGCGACCAAGCTGCTTACAGGTTGCC 195022
QY 304 AACTACATTATGCAATTAACCAAGCTTGCCTCCCAAGCAAGCTGCTTCCGTTATTCGCGCT 363
DB 195021 AACCTAGAAATTTGCAATGATGCACTGATCAAGACCAACATCCGACGTGCTG 194962
QY 364 ATGAGTTGACCAAAACGTTTGAAGACGCGACGAATTCACAGTACCGTCTTCCGCC 423
DB 194961 ATAGACTTCAAGCAATTAAGTCAACGCGAAACATCAACGCCAACTATTAAGCGCTC 194902
QY 424 CTCGATGAAGCCCGCGGCTTGGGCTGTGAAGTCTCCCTTACGAATCAAGGATTTG 483
DB 194901 GTGAGCAACGCGACCAAGCCCGTGGGAGTGAAGTCACTGTATGATATCAAGACATT 194842
QY 484 GTTCCGCGCAAGAAATCCTTGCGCAATGACAGGACAAATTAACCGCGCAACGCGAAAA 543
DB 194841 CAGCCACGCGATTAATCTGCGCGATGTCATGACCAACAAAGATGCTGAACAAACGAG 194782
QY 544 CGCGCCGCTATTTCCGAATCCGAAGCGGTAATTCGAACAAATCAACCTTCCAGTGT 603
DB 194781 CGTGCAACATCTTGAAGCGGAGGAGTACGCCAATCGGCAATCTTGTGCTCGCATGCT 194722
QY 604 CAGCGTGAAGCCGAATTCACAAATTCGAAGGCGAGGCTCAGGCTCGGTCAATGCTGCC 663
DB 194721 GAGAAAGCAAGCCCGCTGATGAGAGCGCAAGGCGCAAGAAACCGCATTCGTTATGCA 194662
QY 664 AATGC 668
DB 194661 GAAAC 194657

RESULT 24

US-10-425-114-2660
; Sequence 2660, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2660
; LENGTH: 852
; TYPE: DNA
; ORGANISM: *Zea mays*
; OTHER INFORMATION: Clone ID: LIB4570-005-G12_FLI
US-10-425-114-2660

Query Match 15.6%; Score 148.2; DB 18; Length 852;
Best Local Similarity 55.0%; Pred. No. 4.3e-39;
Matches 231; Conservative 0; Mismatches 238; Indels 0; Gaps 0;
QY 60 CGTCATCCCCCAGCAGAGATCCACGTTGTGCAAGAGCTCGGCGTTTCATCGCCGCT 119
DB 310 CATAGTCCGAGAGAGAGGCTTACGTTGTGAGAGATTCCGGAAGTATCTCAAGACCTT 369

QY 485 TTCGCCGCGAAGAAATCTCTGCGCGAATGCGACACAAATTAACCGCGCGAAGCGGAAAAAC 544
DB 247 ATCTCCGACGAGGGATTAGCGAGGCTATGAGATGACAGCGCTGAGGACAGAAAGAAAAAC 306
QY 545 GCGCCCGATTGCGCGAATCCGAAAGCGCGTAAATGAAATCAACCTTGGCAGTGGTC 604
DB 307 GCGCTCAATCTTGTAGTCAAGAGGAGTAAA----- 338
QY 605 AGCGTGAAGCGGAAATCCAAACATCCGAGCGGCTCAGCGCTCGGTCATTCGCTCA 664
DB 339 -----CAGGCCCAATTCCTTGAATCAGAAAGGAAAAAGCTGCCAGATCTTGTATCTG 393
QY 665 ATGCGGAGAAATCGCGCGCATCAACCGCGCCAAAGGCGAGCGGAATTCCTGCGCTTG 724
DB 394 AAGGAGCTATGTTGATCTAGCAAAACCGTCCAGAGGTGCGGCTGAGCAATTCCTTGCA 453
QY 725 TTGCGGAGCGCAATGCCAAGCCATCCGTCATTTGCGCGCGCGCTTCAAAACCGAAGGC 784
DB 454 AGTCAGAAAGCTACTGCTCGTGAATGAGATTGGTTTCAAGATGACATCTGAAGGCA 513
QY 785 GCGCGGATGCGGTCATCTGAATTTGCGGAAACAATACCTAGCGCGCTTCAACAATCTTG 844
DB 514 GTGCCAAGGCTGCTAGCGCTGAACCTTGAGAGCAATACATCGAAGCATTCGAATCTGG 573
QY 845 CCAAGAAAGCAATACGCTGATTTATGCCCGCCCAATGTTGCC 885
DB 574 CACAAAGCAATACATGCTTCTTCCAGGTGATAGTCC 614

RESULT 27

US-10-437-963-7661
; Sequence 7661, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 7661
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76636C.1
US-10-437-963-7661

Query Match 13.4%; Score 126.8; DB 19; Length 727;
Best Local Similarity 55.8%; Pred. No. 7.6e-32;
Matches 242; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
QY 60 CGTCATCCCGCAGCAGAGTCCAGCTGTGTCAAGAGCTCGGCGCTTCCTCATCGCGCT 119
DB 246 CATCGGCGGAGAAAGAGCGTTCTGTGTGAGCGGTTCTGGCAAGTACGTCAAGAGCT 305
QY 120 GACGCGCGGTTCGAATTTTGAATTCCTTTATCGACCGCGTGCCTTACCGCATCTGCT 179
DB 306 CGGCTCCGGAGATCCAGTCTGCTCCCTCGTGAACGCGATCGCTACGCTCGCT 365
QY 180 GAAAGAAATCTCTTGAAGTACGTAACGACGAGTCTCATCAGCGCGATTAATACGANT 239
DB 366 CAGGAGAGGAGCATCCCATCCCGACAGATCCGCAATCAAGAGCAACGCTCCCAT 425

QY 240 GACTGTGACGCGCATCATCTATTTCAGTAACGATCCAAATCGCTCATACGTTG 299
DB 426 CCAATGACGCGCGCTCTTACGTACAGATTGTGATCTCTTACCTTGTCTATGAGTGT 485
QY 300 GAGCACTACATTTATGCGAATTAACCGAGCTTGGCCAAACGACGCTGCTTATGCG 359
DB 486 GAGAAATCAATTTTTCAGTCAATACAGCTTGGCCAAACATATGAGAAAGTACGCTGG 545
QY 360 GCGTATGAGATTCGACAAACGTTTGAAGACGAGCAATCAACGTAACGCTGCTC 419
DB 546 AAGATTAACGTAGCAAGACTTTTGAAGAGGAGATACATAATGAGCAATTTGAG 605
QY 420 CGCCCTCGATGAAGCGCGGCGCTTGGGCTGTGAAGTCTCTCGTTAGAAATAGGA 479
DB 606 GTCCATTAATGAGCTGCAACTGATTTGGGAGCTGAAATGCTCTTATGAGATCAGGA 665
QY 480 TTTGGTCCGCGC 493
DB 666 TATATCTCGGCAC 679

RESULT 28

US-09-878-134-349
; Sequence 349, Application US/09878134
; Publication No. US20020086303A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon B.
; APPLICANT: Xu, Jianshun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 21021.532
; CURRENT APPLICATION NUMBER: US/09/878,134
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 349
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-878-134-349

Query Match 13.4%; Score 126.8; DB 9; Length 732;
Best Local Similarity 49.7%; Pred. No. 7.6e-32;
Matches 323; Conservative 0; Mismatches 327; Indels 0; Gaps 0;
QY 85 GTTTCGAAAGGCTCGGGGCTTTCATCGCGCGCTGACGCGCGTTTGAATTTTGAAT 144
DB 6 GTGTGAGCGGATGAGCGCGGATTCACCGGATCTCGAGCGCTGTTGAACATCTCATC 65
QY 145 CCTTTATCGACCGGCTGCTACCGCATTCGCTGAAGAAATCTTTTAAAGTACCC 204
DB 66 CCGTGTATGACCGGATCGATATGTCAGAGTCTCAAGAAATTTGTCAACGCGCT 125
QY 205 ACCGAGGTTCATCAGCGCGCATTAATACGAATTCAGCTGTGAAGCGCATCATTAATTC 264
DB 126 GAGCAGTGGCTGTGATCTTCGACAAATGTAATCTGCAATGAGAGTCTCTTAACCTG 185
QY 265 CAAGTAACGATCCCAACTCGCTCATTCGCTGAGAGCACTAATTAATGCAATTAAC 324
DB 186 CCGATCATGAGACCTTTCAAGGCAAGCTAGGTGTGAGAGACCTGAGATGCCGATC 245
QY 325 CAGCTTGCCAAACGACGCTGCTTCTGTTATCGGCGGTATGAGAGTGAACAAACGTTT 384
DB 246 CAGCTAGCTCAAAACCATGAGATCAGAGCTCGGCAAACTCTCTGGAACAAAGTCTTC 305
QY 385 GAAAGACGGAAGAAATCAACGTAACGTCCTGCTCCCTCGATGAGAGCGCGCGGCT 444
DB 306 CGGAAACGGAATCTCTGAATGACGATTTGAGATGCAATACCAAGCTCTGACTGC 365
QY 445 TGGGGTGAAGTCTCTCGCTACGAAATCAAGATTTGATTCCGCGCAAGAAATCTCT 504

Db 366 TGGGATATCCGTCGCTCCGTTATGATGATCAAGATATCCATGTGCAACCCCGGGTGA 425
Qy 505 CGCCCAATGACGACCAATTAACCGCCGAAGCCAAAACGCGCCGATATGCCGAATCC 564
Db 426 GAGTCTATGACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 485
Qy 565 GAAAGCCGTAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 624
Db 486 GAGGGAGCCGAGAGTGGCCATCATGTGCAAGAGGAAAGAAACAGGCCAGATCTG 545
Qy 625 CAATCCGAGGAGGAGTCCAGGCTGCGTCAATGCGTCAATGCCGAGAAATGCCCC 684
Db 546 GCTTCGGAAGCAAGAAAGCTGAACAGTAATCAGGAGAGAGAGAGAGAGAGAG 605
Qy 685 ATCAACGCGCCGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 734
Db 606 CTGGCAAGGCGCAAGGCTAAAGCTGAAGCTATGCAATCTGGCTGACG 655

RESULT 29

US-10-767-701-5816
; Sequence 5816, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 5816
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(742)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MA03-CLUS25744_1
US-10-767-701-5816

Query Match 13.2%; Score 124.8; DB 19; Length 742;
Best Local Similarity 55.1%; Pred. No. 3.7e-31;
Matches 243; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

Qy 60 CGTATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 119
Db 297 CATAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 356
Qy 120 GAGCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 179
Db 357 CGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416
Qy 180 GAAAGAAATCCCTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 239
Db 417 CAAG 476
Qy 240 GACTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 299
Db 477 ACAGATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 536
Qy 300 GAGCAATCAATTAATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAGCAAT 359
Db 537 GGAAGATCAATTAATGAGCAATTAATGAGCAATTAATGAGCAATTAATGAGCAAT 596
Qy 360 GCGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 419
Db 597 GAAATTAACCTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656

Qy 420 CGCCCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
Db 657 TGCCATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716
Qy 480 TTTGCTTCGCGCCGAGAGAAAT 500
Db 717 CATTAATCTTCCTCAATAGGAGAT 737

RESULT 30

US-10-425-114-19667
; Sequence 19667, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19667
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-091-G4_FLI
US-10-425-114-19667

Query Match 12.3%; Score 117; DB 18; Length 1091;
Best Local Similarity 51.9%; Pred. No. 2e-28;
Matches 316; Conservative 0; Mismatches 260; Indels 33; Gaps 1;

Qy 277 CCCAACTCGCCCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 336
Db 2 CCTACCTTCTCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
Qy 337 ACGAGCGTGGCTTCGTTATCGGCGTATGAGGAGGAGGAGGAGGAGGAGGAGGAG 396
Db 62 ACAACATGAGAGAGTGAAGTGGAGAGATTAAGTAAAGATTTGAGAGAGAGAT 121
Qy 397 GAAATCAACAGTACCGTCTCCGCTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 456
Db 122 GCATTAATGAGAAATTTGAGTGCATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
Qy 457 GTCCGCTTACGAAATCAAGATTTGATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 516
Db 182 TGATTCGCTATGAGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
Qy 517 GCACAAATTAACCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 576
Db 242 ATGAGGCTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301
Qy 577 ATGCAAAATCAACTTTCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636
Db 302 -----CAGGCCCAAAATCTTGAATCAAGAGG 328
Qy 637 GAGGCTCAGGCTGGGCTCAATGAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 696
Db 329 AAAAAAGTGGCCAGATCTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 388
Qy 697 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 756
Db 389 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 448
Qy 757 ATTGCGCGCCCTTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 816
Db 449 GTTTCAGATGAGAGCAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508

QY 817 CAAATGTAAGCCGCTTGAACATCTTGGCAAGAAAGCATACCTGATTTATGCCCC 876
DB 509 CAAATGTAAGCAAGCATCTTCAATCTGGACAAAAGACAAATACATGCTTCCAGAGT 568
QY 877 AATGTTGCC 885
DB 569 GATAGTGCC 577

RESULT 31

US-09-922-217-1031
; Sequence 1031, Application US/09922217
; Patent No. US20020764141
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Jiang, Yudi
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1031
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 443
; OTHER INFORMATION: n = A,T,C or G
US-09-922-217-1031

Query Match 11.7%; Score 111.2; DB 9; Length 518;
Best Local Similarity 51.8%; Pred. No. 1.3e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 85 GTTGTGAAAGCTCGGGGCTTTCATCGCGCCCTGACGCGCGGTTGAAATTTTGATT 144
DB 6 GTGTGTGAGCGAATGGCCGATTCACCGAGTCTTGAGCCTGTGTAACATCTCTCATC 65
QY 145 CCTTATGACCGCGCTGCTACCGCATTTGCTGAAAGAAATCCCTTTAGACGTACC 204
DB 66 CTTGTGTAGCCGATCGGATGCGATGTCAGAGTCTTAAGAAATTTGTCATCAACGTGCT 125
QY 205 AGCCAGTCTGATCAACGCGCGATTAATGCAATTGATCTGTGACGCACTATTTTC 264
DB 126 GAGCAGTGGCTGTGATCTTCGACATGTAACCTGCAATGATGAGAGTCTTTACCTG 185
QY 265 CAAGTAACCGATCCAACTCGCTCATACGTTGACGAACTACATTAATGGCAATTACC 324
DB 186 CCATCATGAGCCCTTAACAGGCAAGCTACGCTGTGAGAGACCTGATGATGCGCTCAC 245
QY 325 CAGCTTGCACCAACGAGCGCTGCTGCTTATGCGCGATGAGATTGCAAAAGTTT 384
DB 246 CAGCTAGCTCAACCAACATGATGAGCTGCGAAACTCTCTTGAACAAAGTCTTC 305
QY 385 GAAGAACGAGCAAAATCAACAGTACCGTCTCCGCTCGATGAAGCGCGGAGCT 444
DB 306 CCGGAACGGAGATCCTTGAATGCAAGATTTGAGATGATCAACAAAGTGTGACTGC 365
QY 445 TGGGATGTAAAGTCTCCGTTACGAATACAGAAATTTGTTCCGCGCAAGAAATCTT 504

DB 366 TGGGATTCGCCCTGCTCGTTATGATCAAGATATCAATGTCACCCCGGTGAAA 425
QY 505 CGCGCATGACAGGCAAAATTAACGCGCGAAGCGGAAACGCGCGCTGATGCGCAATCC 564
DB 426 GAGTCTATGACAGATGATGAGGAGGAGGCGGAAACGCGCGACAGTTCTAGAGTCT 485
QY 565 GAAG 569
DB 486 GAGGG 490

RESULT 32

US-09-833-263-1031
; Sequence 1031, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1031
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(518)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-1031

Query Match 11.7%; Score 111.2; DB 9; Length 518;
Best Local Similarity 51.8%; Pred. No. 1.3e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 85 GTTGTGAAAGCTCGGGGCTTTCATCGCGCCCTGACGCGCGGTTGAAATTTTGATT 144
DB 6 GTGTGTGAGCGAATGGCCGATTCACCGAGTCTTGAGCCTGTGTAACATCTCTCATC 65
QY 145 CCTTATGACCGCGCTGCTACCGCATTTGCTGAAAGAAATCCCTTTAGACGTACC 204
DB 66 CTTGTGTAGCCGATCGGATGCGATGTCAGAGTCTTAAGAAATTTGTCATCAACGTGCT 125
QY 205 AGCCAGTCTGATCAACGCGCGATTAATGCAATTGATCTGTGACGCACTATTTTC 264
DB 126 GAGCAGTGGCTGTGATCTTCGACATGTAACCTGCAATGATGAGAGTCTTTACCTG 185
QY 265 CAAGTAACCGATCCAACTCGCTCATACGTTGACGAACTACATTAATGGCAATTACC 324
DB 186 CCATCATGAGCCCTTAACAGGCAAGCTACGCTGTGAGAGACCTGATGATGCGCTCAC 245
QY 325 CAGCTTGCACCAACGAGCGCTGCTTATGCGCGATGAGATTGCAAAAGTTT 384
DB 246 CAGCTAGCTCAACCAACATGATGAGCTGCGAAACTCTCTTGAACAAAGTCTTC 305
QY 385 GAAGAACGAGCAAAATCAACAGTACCGTCTCCGCTCGATGAAGCGCGGAGCT 444
DB 306 CCGGAACGGAGATCCTTGAATGCAAGATTTGAGATGATCAACAAAGTGTGACTGC 365
QY 445 TGGGATGTAAAGTCTCCGTTACGAATACAGAAATTTGTTCCGCGCAAGAAATCTT 504
DB 366 TGGGATTCGCCCTGCTCGTTATGATCAAGATATCAATGTCACCCCGGTGAAA 425
QY 505 CCGCATGACAGGCAAAATTAACGCGCGAAGCGGAAACGCGCGCTGATGCGCAATCC 564
DB 426 GAGTCTATGACAGATGATGAGGAGGAGGCGGAAACGCGCGACAGTTCTAGAGTCT 485

OY 565 GAAG 569
DB 486 GAGG 490

RESULT 33

US-10-025-380-1031
Sequence 1031, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025.380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1031
LENGTH: 518
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 443
OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1031

Query Match 11.7%; Score 111.2; DB 13; Length 518;
Best Local Similarity 51.8%; Pred. No. 1.3e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

OY 85 GTTGTGAAAGGCTCGGGCGTTTCCATCGCGCCCTGACGGCGGTTTGAATATTTGATT 144
DB 6 GTGGTGAAGCGAATGGGCGAATTCACCGGATCTCGAGCGCTGGTTGAACATCCTCATC 65
OY 145 CCTTTATGACCGCGTGGCTTACCGCAATTCGCTGAAGAAATCCCTTTAGAGTACC 204
DB 66 CCGTGTGTAAGCCGGATCGAATGTGCAAGATCTCAAGAAATTTGTCATCAACGTGCT 125
OY 205 AGCCAGGTCTGATCAGCGGGGATTAATAGCAATTTGACTGTGAGCGCATCATTTTC 264
DB 126 GAGCAGTGGCTGTACTCTGACAAATGTAATCTGTCAATGATGAGTCTTTTACTG 185
OY 265 CAAGTAACCGATCCCAACTGCGCTCATACGTTTCAGCAACTATCATTTATGCAATTAAC 324
DB 186 CGCATCATGAGACCTTACAGGCAAGCTACGGTGTGAGAGACCGTGAATATGCGTACC 245
OY 325 CAGCTTGCCCAAGCAGCGCTGCTTCCGTTATCGGGCGTAATGAGTTGACAAAAGTTT 384
DB 246 CAGTAGCTCAAAACAACCATGATCAGAGCTCGGCAAACTCTCTGTGCAAAAGTCTTC 305
OY 385 GAAGAAGCGAGCAAAATCAACAGTACCGTCTCCCGCCCTGATGAGAGCGCGCGGCT 444
DB 306 CGGAAACGGAGTCCCTTAATGCGCAATGTGATGATCAATCAAGAGTGTGACTGC 365
OY 445 TGGGGTGAAGAGTCTCCGTTACGAATCAAGATTGGTTCCGCGCAAGAAATCCTT 504

DB 366 TGGGGTATCCGCTCTCCGTTATGATCAAGGATATTCATGAGCCACCCGGGTAAA 425
OY 505 CGCCATGACAGGCAAAATTAACCGCGAAGCCAAAAGCGCCGATATGCGGAATCC 564
DB 426 GAGTCTATGACAGATGATGAGAGGAGCGGCGAAGCGGCCACAGTTCTAGACT 485
OY 565 GAAG 569
DB 486 GAGG 490

RESULT 34

US-09-998-598-841
Sequence 841, Application US/0998598
Patent No. US20020150922A1
GENERAL INFORMATION:

APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998.598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corlixa Invention Disclosure Database
SEQ ID NO 841
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
US-09-998-598-841

Query Match 11.7%; Score 110.6; DB 9; Length 504;
Best Local Similarity 51.8%; Pred. No. 2e-26;
Matches 251; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

OY 85 GTTGTGAAAGGCTCGGGCGTTTCCATCGCGCCCTGACGGCGGTTTGAATATTTGATT 144
DB 6 GTGGTGAAGCGAATGGGCGAATTCACCGGATCTCGAGCGCTGGTTGAACATCCTCATC 65
OY 145 CCTTTATGACCGCGTGGCTTACCGCAATTCGCTGAAGAAATCCCTTTAGAGTACC 204
DB 66 CCGTGTGTAAGCCGGATCGAATGTGCAAGATCTCAAGAAATTTGTCATCAACGTGCT 125
OY 205 AGCCAGGTCTGATCAGCGGGGATTAATAGCAATTTGACTGTGAGCGCATCATTTTC 264
DB 126 GAGCAGTGGCTGTACTCTGACAAATGTAATCTGTCAATGATGAGTCTTTTACTG 185
OY 265 CAAGTAACCGATCCCAACTGCGCTCATACGTTTCAGCAACTATCATTTATGCAATTAAC 324
DB 186 CGCATCATGAGACCTTACAGGCAAGCTACGGTGTGAGAGACCGTGAATATGCGTACC 245
OY 325 CAGCTTGCCCAAGCAGCGCTGCTTCCGTTATCGGGCGTAATGAGTTGACAAAAGTTT 384
DB 246 CAGTAGCTCAAAACAACCATGATCAGAGCTCGGCAAACTCTCTGTGCAAAAGTCTTC 305
OY 385 GAAGAAGCGAGCAAAATCAACAGTACCGTCTCCCGCCCTGATGAGAGCGCGGCT 444
DB 306 CGGAAACGGAGTCCCTTAATGCGCAATGTGATGATCAATCAAGAGTGTGACTGC 365
OY 445 TGGGGTGAAGAGTCTCCGTTACGAATCAAGATTGGTTCCGCGCAAGAAATCCTT 504
DB 366 TGGGGTATCCGCTCTCCGTTATGATCAAGGATATTCATGTGCAACCCGGGTGAAA 425
OY 505 CGCCATGACAGGCAAAATTAACCGCGAAGCCAAAAGCGCCGATATGCGGAATCC 564
DB 426 GAGTCTATGACAGATGATGAGAGGAGCGGCGAAGCGGCCACAGTTCTAGAGTCT 485
OY 565 GAAG 569
DB 486 GAGG 490

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RESULT 35
US-09-998-598-58
; Sequence 58, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Megher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 58
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-58

Query Match      11.6%; Score 110.4; DB 9; Length 563;
Best Local Similarity 53.5%; Pred. No. 2.5e-26;
Matches 231; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY      62 TCATCCCCGAGGAGGAGTCCAGCTGTGAAAGGCTCGGGCGTTCCATCGGCCCTGA 121
DB      124 TCGTGGCGGAGGAGGCGCTGGGTGTGAGAGGAATGGGCCGATTCCACCGGATCTGG 183
QY      122 CGCGCGGTTGAATATTTGATTCCCTTTATCGACCGCGTCCGCTTACCGCATTCGCTGA 181
DB      184 AGCTGGTTGAACATCTCATCTCGTGTGAGACCGGATTCGATATGTGAGAGTCTCA 243
QY      182 AAGAAATCCCTTTAGACGTACCCAGCTGTGCATCGACGGCGGATATAGCAATTTGA 241
DB      244 AGGAATTTGTCAACAGTGGCTGAGCACTCGGCTGTGACTTCGCAATGTAACTCTGC 303
QY      242 CGTTGAGCGGCATCATCTATTTCAGATTAACGATCCCAACTCGGCTCATACGTTTGA 301
DB      304 AATTCATGAGTCTCTTACCTGCGCATATGAGACCTTTCAAGGACGATACGATGTGG 363
QY      302 GCAACTACATTATGCAATTACCCAGCTTGCCCAAGCAAGCTGCTGCTTATCGAGC 361
DB      364 AGGACCTGAGTATGCGTCAACCACTAGCTCAAAACACATGATCAGAGCTCGGA 423
QY      362 GTATGAGTTGACAAACGTTGAAGAACGACGAAATCAACAGTACCGTGTCTCG 421
DB      424 AACTCTCTCGCAAGTCTTCCGGAAACGGAGTCCCTGAATGCGAGCATTTGTGATG 483
QY      422 CCTCATGAGCGCGCGGGCGCTTGGGGTGTGAATCTCCGTTTGAATCAAGGATTT 481
DB      484 CCATCAACCAAGTGTGACTGCTGTGAGTCCGCTGCTCGTTATGATCAAGATTA 543
QY      482 TGGTTCGCGCGC 493
DB      544 TCCATGTGCCAC 555

RESULT 36
US-10-198-846-13409
; Sequence 13409, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steilmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
```

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; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13409
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1149..1150
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13409

Query Match      11.6%; Score 110; DB 14; Length 1150;
Best Local Similarity 49.4%; Pred. No. 5e-26;
Matches 345; Conservative 0; Mismatches 320; Indels 33; Gaps 1;

QY      218 TCACGCGGATTAATGCAATTTGACTGTGACGGCATCATTTTCCAAAGTACCAGATC 277
DB      127 TGACTCTGACATGTAATCTGTGCAAAATGATGAGTCTTTTACCTGCGCATCATGAGCC 186
QY      278 CCAACTCGGCTTCATACGCTTGCAGCACTACATTATGGCAATTAACGAGTTGCCAAA 337
DB      187 CTTAACGAGCAAGCTACGCTGTGGAGACCTGAGTATGCGTCAACGAGTCTCAAA 246
QY      338 CGACGCTGCTTCCTTTATCGGGCGTATGAGTTGAGCAAAAAGTTTGAAAGACGAGC 397
DB      247 CAACATGATGATCAAGCTTCGGCAAACTCTCTGTGACAAATCTTCGGGAAACGAGAT 306
QY      398 AATTAACAGTACGCTGTCTCCGCTTGATGAAGCCGCGGCTTGGGTGTGAAG 457
DB      307 CCTGAATGCCAGACTTGTGATGATCAACCAAGCTGTGATCTGGGGTATCCGCT 366
QY      458 TCTCTCGTTAGCAATTCAGGATTTTGTTCGCGCCCAAGAAATCTTCGCGCAATGACAG 517
DB      367 GCTCTCGTTATGATCAAGATTAATCAATGTCACCCCGGTGAAGAGTTATGACA 426
QY      518 CACAATTATCGCGCGAAGCGGAAACGCGCCGCTATTGCGCAATCCGAAGCCGTAAA 577
DB      427 TCGAGTGAAGCAAGCGCGGAAACGCGCCAGCTTCTAAGTCTGA----- 475
QY      578 TCGAAACAATCAACTTGGCACTGTGACGCTGAAAGCGAAATCCAACATCCGAAGCGC 637
DB      476 -----GGGGAACCGAGAGTCCGCAATCAATGTGCAAGAGGGA 513
QY      638 AGCTCAGGCTGCGTCAATGCTTCAATGCGGAGAAATCCCGGCATCAACCGGCGCA 697
DB      514 AGAAACAGGCCCAAGTCTTGCGCTCGAAGCAAGAAAGGCTAACAAGATTAATCAGGCA 573
QY      698 AAGGCGAAGCGGAATCCCTGCGCTTGTGTGCGAAGCCCAATCCGAAGCCATCCGTCAA 757
DB      574 CAGAGAGGCGCAGTGCATGTTCTGCGAAGGCCAAGGCTTAAGCTAAGCTATTCCAAATCC 633
QY      758 TTGCGCGCGCTTCAAAACCAAGGCGGCGAGATGCGGTCAATCTGAAGATTGCGGAAC 817
DB      634 TGGCTGCACTCTGACACAAATTAATGAGATGACAGCACTTCACTGACTGTGCGGAGC 693
QY      818 AATAGCTAGCCGCGTTCAACATCTTGGCAAGAAAGCAATAGCGTGAATTAATGCGCGCA 877
DB      694 AGTATGTACGCGGTTCTCAAACTGCGCAAGAGCTTCAACACTATCTACTGCGCTTCA 753
QY      878 ATGTGCGGACATCGGCAAGCTGATTTCTGCGGCGAGT 915
DB      754 ACCCTGCGATGTACACAGCATGTGTGCTCAGGCAATG 791

RESULT 37
US-09-815-343-1428
; Sequence 1428, Application US/09815343
```



```
Patent No. US20010055396A1
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1428
LENGTH: 691
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(691)
OTHER INFORMATION: n = A,T,C or G
US-09-815-343-1428
```

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Query Match 10.2%; Score 96.4; DB 9; Length 691;
Best Local Similarity 52.8%; Pred. No. 1.6e-21;
Matches 208; Conservative 0; Mismatches 186; Indels 0; Gaps 0;
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OY 85 GTGTGCAAGAGCTCGGGCGTTTCATCGCCCTGAGCGCGGGTTGAAATTTGATT 144
DB 6 GTGTGAGAGCAATGGGCCGATTCACCGGATCTCGAGCGCTTGTTAAACATCTCTATC 65
OY 145 CCTTTATGACCGCGCTGACCTACCGCAATTCGCTGAAAGAAATCCCTTTAGACGTAACC 204
DB 66 CCGTGTATGACCGGATCGGATATGTGCAAGATCTCAAGAAATGTGATCAAGCTGCT 125
OY 205 AGCCAGGCTGATACCGCGGATATATGCAATTTGATCTGAGCGGATCATCTATTC 264
DB 126 GAGCAGTCGCGTGTACTCTGACAAATGTAATCTGCAAAATGATGAGTCTTTACCTG 185
OY 265 CAAGTAACCGATCCCAACTCGCTCATACGTTGAGCAACTATATGAGCAATTAC 324
DB 186 CGCATATGAGACCTTTACAGGCAAGCTACGTTGAGAGACCCGAGATATCCGTCACC 245
OY 325 CAGCTTGGCCAAACGACGCTGCGTTCCGTTATCGGGCGTATGAGATTGACAAAACGTTT 384
DB 246 CAGTAGTCAAAACCAACATGATGACAGCTCGGCAAACTCTCTGCAAAAGTCTTC 305
OY 385 GAAGAACCGGAGCAATCAAGTACCGTCTCTCCGCTTGAAGACCGCGGGCT 444
DB 306 CGGGAACGGAGTCCCTGAATGCCAGATTTGGATGATCAACCAAGCTGCTACTGC 365
OY 445 TGGGGTGTAAAGTCTCCGTTACGAATCAAG 478
DB 366 TGGGTATCCGCTCGCTCGTTATGATCAAG 399
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RESULT 38
US-10-097-105-1428
Sequence 1428, Application US/10097105
Publication No. US20040037842A1
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine Joy
APPLICANT: King, Gordon E.
APPLICANT: Secrist, Heather
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.504C1
CURRENT APPLICATION NUMBER: US/10/097,105
NUMBER OF SEQ ID NOS: 1562
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1428
```

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LENGTH: 691
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 439, 508, 523, 526, 539, 561, 575, 582, 584, 602, 614, 623,
LOCATION: 626, 645, 648, 664
OTHER INFORMATION: n = A,T,C or G
US-10-097-105-1428
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Query Match 10.2%; Score 96.4; DB 18; Length 691;
Best Local Similarity 52.8%; Pred. No. 1.6e-21;
Matches 208; Conservative 0; Mismatches 186; Indels 0; Gaps 0;
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OY 85 GTGTGCAAGAGCTCGGGCGTTTCATCGCCCTGAGCGCGGGTTGAAATTTGATT 144
DB 6 GTGTGAGAGCAATGGGCCGATTCACCGGATCTCGAGCGCTTGTTAAACATCTCTATC 65
OY 145 CCTTTATGACCGCGCTGACCTACCGCAATTCGCTGAAAGAAATCCCTTTAGACGTAACC 204
DB 66 CCGTGTATGACCGGATCGGATATGTGCAAGATCTCAAGAAATGTGATCAAGCTGCT 125
OY 205 AGCCAGGCTGATACCGCGGATATATGCAATTTGATCTGAGCGGATCATCTATTC 264
DB 126 GAGCAGTCGCGTGTACTCTGACAAATGTAATCTGCAAAATGATGAGTCTTTACCTG 185
OY 265 CAAGTAACCGATCCCAACTCGCTCATACGTTGAGCAACTATATGAGCAATTAC 324
DB 186 CGCATATGAGACCTTTACAGGCAAGCTACGTTGAGAGACCCGAGATATCCGTCACC 245
OY 325 CAGCTTGGCCAAACGACGCTGCGTTTCGTTATCGGGCGTATGAGTTGACAAAACGTTT 384
DB 246 CAGTAGTCAAAACCAACATGATGACAGCTCGGCAAACTCTCTGCAAAAGTCTTC 305
OY 385 GAAGAACCGGAGCAATCAAGTACCGTCTCTCCGCTTGAAGACCGCGGGCT 444
DB 306 CGGGAACGGAGTCCCTGAATGCCAGATTTGGATGATCAACCAAGCTGCTACTGC 365
OY 445 TGGGGTGTAAAGTCTCCGTTACGAATCAAG 478
DB 366 TGGGTATCCGCTCGCTCGTTATGATCAAG 399
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RESULT 39
US-09-969-034-3476
Sequence 3476, Application US/09969034
Publication No. US20040110668A1
GENERAL INFORMATION:
APPLICANT: Burgess, Christopher C.
APPLICANT: Askle, Jon H.
APPLICANT: Carroll, Eddie III
APPLICANT: Carino, Theodore J.
APPLICANT: Dwivedi, Poornima
APPLICANT: Molino, Gary A.
APPLICANT: Thagalingam, Arunthathi
APPLICANT: Lewis, Marcia E.
TITLE OF INVENTION: Nucleic Acid Sequences Differentially
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
PRIOR APPLICATION NUMBER: 60/237,271
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3476
LENGTH: 683
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 466, 484, 511, 517, 524, 542, 546, 549, 582, 604, 611, 617,
LOCATION: 651, 660, 666, 680, 683
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OTHER INFORMATION: n = A,T,C or G
US-09-969-034-3476

Query Match 10.1%; Score 95.6; DB 11; Length 683;
Best Local Similarity 53.3%; Pred. No. 3e-21;
Matches 223; Conservative 0; Mismatches 194; Indels 1; Gaps 1;

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QY 62 TCATCCCCCAGAGAGAGTCCAGTTCGAAAGGCTCGGGGCTTCCATCCGCGCTTGA 121
DB 9 TCGTCCCGCAGAGAGGCGCTGGGTGTGAGCGATGCGCGATTCGCCGATCTCG 68
QY 122 CGGCGGCTTGAATTTTGAATTCCTTATGACCGCGCTCGCGCTTCCGCAATGCTGA 181
DB 69 ACCCTGGTTGAACATCCATCCATCCCTGTGTGAGCCGATCCGATATGTCAGAGTCTGA 128
QY 182 AAGAAATCCCTTGAAGTACAGCAGCAGCTGTGATCAAGCGCGATTAATGCAATTTGA 241
DB 129 AGGAAATTCATCAACGTCGCTGAGCACTCGGCTGTGACTCTCGAATATGTAACCTTGC 188
QY 242 CTGTGACCGCATCATCTATTTTCAAGTAAACGATCCAACTCGCTCATACGTTTCA 301
DB 189 AATGATGATGAGTCTTTTACGTGCGCATGAGACCTTAAAGGCAAGCATACGCTGTG 248
QY 302 GCAATCACTTATGCAATTAACCAAGCTTGCCTTCCAAAGCGCTGCGCTTATGCGGCG 361
DB 249 AGGACCTGATGATGCGCTGACCGCTGATGCTTAAACCAACATGATGAGAGCTGCGCA 308
QY 362 GTATGAGTTGAGCAAAAGTTTGAAGAAAGCGAGCAAGAAATCAACAGTACGCTGCTCCG 421
DB 309 AACTCTCTGACAAAGTCTTCGGGAAAGGAGAGCCCTGAATGCAAGATTTGTGATG 368
QY 422 CCTCGATGAGCGCGCGGCGCTTGGGGTGTGAAAGT-CCTTCGTTACGAATCAAGG 478
DB 369 CCATCAACCAAGCTGTGACTGCTGGGGTATCCCGCTGCTCGTTATGATGAAAG 426
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RESULT 40
US-09-998-1161/c
; Sequence 1161, Application US/0998598
; Patent No: US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998, 598
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1161
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 615
; OTHER INFORMATION: n = A,T,C or G
US-09-998-598-1161

Query Match 9.7%; Score 91.8; DB 9; Length 622;
Best Local Similarity 48.0%; Pred. No. 5.6e-20;
Matches 258; Conservative 1; Mismatches 278; Indels 0; Gaps 0;

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QY 198 CGTACCAGCAGGTCTGATCAAGCGCGATTAATGCAATGATGTTGACGCGCATCAT 257
DB 614 CGGCGCTGAGAGAGTGGCTGTGACTCTCGAAGTAACTGCAATTCATGATGAGTCTT 555
QY 258 CTATTTTCAAGTAAAGGATCCAAAGTCCGCTCATACGTTGAGAGCAACATTAATGCG 317
DB 554 TTACTGCGCATGAGACCTTTAAGGCAAGCTACGCTGAGAGGAGCCCTGATGATGCG 495
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QY 318 AATTACCGAGTTGCGCAAGAGCGTGCCTTCCGTTATTCGGGCGTATGAGTTGACAA 377
DB 494 CGTACCCAGCTAGCTTAAACCAACCATGATCAGAGCTCGGCAAACTCTCTGTGACAA 435
QY 378 AACGTTGAAAGAACCGAGCAAGAAATCAACGATACCGTGTCTTCGCGCTTGATGAAGCGC 437
DB 434 AGCTTCCGGGAGACGGAGTCCCTGAAATGCCAGCATTTGTGATGCTATCAACCAAGCTGC 375
QY 438 CGGGGCTTGGGGTGTGAAAGTCTCCGTTAGAAATCAAGATTTGTTTCCGCGGCAAGA 497
DB 374 TGACTGTGGGGTATCCGCTGCTCCGTTATGAGATCAAGGATATCCATGTGCCACCCCG 315
QY 498 AATCTTGGCGCAATGACAGGCAAAATTACCGCGAGCGGAAAGCGGCGGATTTGC 557
DB 314 GGTGAAGAGTCTATGAGATGACAGTGAAGGCAAGGCGGAGAACGAGCCAGACTTCT 255
QY 558 CGAATCCGAGGCGCTTAAATTCGAACAAATCAACTTGCAGTGTGACGCTGAAGCGGA 617
DB 254 AGAGTCTGAGGGAGACCGAGAGTCCGCGCATCAATGTGGCAGAAAGGAGAAAGAGGCCA 195
QY 618 AATCCAGAAATCCGAAGGCGAGCTCAGGCTGCGGTCAATGCTCCATGCGGAGAAAT 677
DB 194 GATCTGGGCTCCGAAGCAGAAAGGCTGAACAGATTAATCAGGAGAGAGAGGCGCAG 135
QY 678 CGCCGCGATCAACCGCGCCAAAGCGGCAATCCCTGCGGCTTGTTCGCGAAGC 734
DB 134 TGCAGTTCTGGGAGGCGCAAGGCTTAAAGCTGAAGCTATTGAAATCTTGGCTGCGAC 78
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Search completed: August 14, 2005, 02:02:30
Job time : 784 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 18:32:50 ; Search time 4375 Seconds
(without alignments)
10499.553 Million cell updates/sec

Title: US-10-018-470A-16

Perfect score: 948
Sequence: 1 atggaatttcattcatctt.....gcagcaaacgcgccaataa 948

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmb1:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	948	100.0	948	1	AF235154 Neisseria
2	948	100.0	948	1	AF235155 Neisseria
3	948	100.0	948	1	AF235156 Neisseria
4	948	100.0	948	6	AX043937 Sequence
5	900	94.9	948	1	AF226511 Neisseria
6	900	94.9	948	1	AF226515 Neisseria
7	896.8	94.6	948	1	AF226513 Neisseria
8	896.8	94.6	948	1	AF226512 Neisseria
9	896.8	94.6	948	1	AF226531 Neisseria
10	896.8	94.6	948	1	AF226536 Neisseria
11	896.8	94.6	948	1	AF226537 Neisseria
12	895.2	94.4	948	1	AF226521 Neisseria
13	895.2	94.4	948	1	AF226523 Neisseria
14	895.2	94.4	948	1	AF226533 Neisseria
15	890.4	93.9	948	1	AF226512 Neisseria
16	890.4	93.9	948	1	AF226527 Neisseria
17	890.4	93.9	948	1	AF226541 Neisseria
18	890.4	93.9	948	6	AX043933 Sequence
19	890.4	93.9	948	6	AX043939 Sequence

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	28	877.6	92.6	948	1	AF226522	AF226522 Neisseria
	29	877.6	92.6	948	1	AF226525	AF226525 Neisseria
	30	877.6	92.6	948	1	AF226529	AF226529 Neisseria
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LOCUS	AF235154				
DEFINITION	Neisseria gonorrhoeae strain NG-F62 GNA1220 (gna1220) gene,				
ACCESSION	AF235154				
VERSION	AF235154.1	GI:7274431			
KEYWORDS	complete cds.				
SOURCE	Neisseria gonorrhoeae				
ORGANISM	Neisseria gonorrhoeae				
REFERENCE	1 (bases 1 to 948)				
AUTHORS	Pizza, M., Scariato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Iuzzo, E., Manetti, R., Marchetti, E., Mora, M., Notti, S., Ratti, G., Santini, L., Savino, S., Scarcellini, M., Storni, E., Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blatz, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.				
	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing				
	Science 287 (5459), 1816-1820 (2000)				
TITLE	Neisseria gonorrhoeae				
JOURNAL	Neisseria gonorrhoeae				
MEDLINE	20175756				
PUBMED	10710308				
REFERENCE	2 (bases 1 to 948)				
AUTHORS	Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-FEB-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy				
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Query Match 100.0%; Score 948; DB 1; Length 948;
Best Local Similarity 100.0%; Pred. No. 4.5e-214; Indels 0; Gaps 0;
Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AP235155

LOCUS AP235155 948 bp DNA linear BCT 22-MAR-2000

DEFINITION

Neisseria gonorrhoeae strain NG-SN4 GNA1220 (gna1220) gene,

ACCESSION

AF235155

VERSION

AF235155.1 GI:7274433

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

2 (bases 1 to 948)

Direct Submission

Submitted (16-FEB-2000)

Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 948; DB 1; Length 948;

Best Local Similarity 100.0%; Pred. No. 4.5e-214; Indels 0; Gaps 0;

Matches 948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Neisseria gonorrhoeae strain FA1090 GNA1220 (gna1220) gene,
DEFINITION complete cds.
ACCESSION AF235156 GI:7274435
VERSION AF235156.1
KEYWORDS Neisseria gonorrhoeae
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 948)

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AUTHORS
  Pizza, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,
  Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, B., Capecci, B.,
  Galeotti, C.L., Iuzzo, E., Manetti, R., Marchetti, B., Mora, M.,
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  Tettelin, H., Hood, D.W., Jeffries, A.C., Sandere, N.J., Granoff, D.M.,
  Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
  Identification of vaccine candidates against serogroup B
  meningococcus by whole-genome sequencing
  Science 287 (5459), 1816-1820 (2000)

JOURNAL
  MEDLINE
  PUBMED
  10710308
  2 (bases 1 to 948)
  20175756

REFERENCES
  Pizza, M., Maignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
  Direct Submission
  Submitted (16-FEB-2000) IRIS Immunobiological Research Institute in
  Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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  Query Match 100.0%; Score 948; DB 1; Length 948;
  Best Local Similarity 100.0%; Pred No. 4,5e-214; Gaps 0;
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ACCESSION AX043937
VERSION AX043937.1 GI:11342858
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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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RESULT 5
AF226511 948 bp DNA linear BCT 11-MAR-2000
LOCUS AF226511
DEFINITION Neisseria meningitidis strain 1000 membrane protein GNA1220
ACCESSION AF226511
VERSION AF226511.1 GI:7228851
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 948)
Pizza, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
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 JOURNAL
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 Neisseria meningitidis
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 1 (bases 1 to 948)
 Pizze, M., Scariato, V., Masignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B.,
 Galeotti, C.L., Iuzzi, B., Manetti, R., Marchetti, E., Mora, M.,
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 Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 2 (bases 1 to 948)
 Pizze, M., Masignani, V., Comanducci, M., Tettelin, H., and Rappuoli, R.
 Direct Submission
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
 JOURNAL
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 JOURNAL
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ORIGIN

Query Match 94.9%; Score 900; DB 1; Length 948;

Best Local Similarity 96.8%; Pred. No. 1.1e-202;

Matches 918; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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AF226513
VERSION
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 948)
Piazza, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B.,
Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M.,
Nuti, S., Rati, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
Tetzelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
Venier, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)
20175756
JOURNAL
MEDLINE
PUBMED
2 (bases 1 to 948)
Piazza, M., Maignani, V., Comanducci, M., Tetzelin, H. and Rappuoli, R.
Direct Submission
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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 Version AF226528.1 GI:7228884
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 Organism Neisseria meningitidis
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 Authors Pizzo, M., Scariato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capechi, B., Galeotti, C.L., Iuzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Scorni, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappelli, R.
 Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

Journal MEDLINE
 PubMed 10710308
 Reference 2 (bases 1 to 948)
 Authors Pizzo, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappelli, R.
 Title Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

Journal
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 Best Local Similarity 96.6%; Pred. No. 6.3e-202;
 Matches 916; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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RESULT 9
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 LOCUS Neisseria meningitidis strain NG3/88 membrane protein GNA1220
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 ACCESSION AF226531
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 KEYWORDS
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
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 1 (bases 1 to 948)
 Pizzo, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,
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 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)
 JOURNAL MEDLINE 20175756
 PUBMED 10710308

REFERENCE 2 (bases 1 to 948)
 AUTHORS Pizzo, M., Maignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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 Best Local Similarity 96.6%; Pred. No. 6.3e-202;
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RESULT 10 948 bp DNA linear BCT 11-MAR-2000
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 LOCUS Neisseria meningitidis strain NGH15 membrane protein GNA1220
 DEFINITION (gna1220) gene, complete cds.
 ACCESSION AF226536
 VERSION AF226536.1 GI:7228900
 KEYWORDS
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 ORGANISM
 Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.
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 Pizza, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capocchi, B.,
 Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., More, M.,
 Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
 Zuo, P., Broecker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 2 (bases 1 to 948)
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 Direct Submision
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
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RESULT 11
AF226537
LOCUS AF226537
DEFINITION *Neisseria meningitidis* strain NGH6 membrane protein GNA1220
(gna1220) gene, complete cds.
AF226537
VERSION AF226537.1 GI:7228902
KEYWORDS
SOURCE *Neisseria meningitidis*
ORGANISM *Neisseria meningitidis*
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; *Neisseria*.
REFERENCE
AUTHORS Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Barolini E., Capecci B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M.,
Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Stormi E.,
Zuo P., Brooker M., Hundt E., Knapp B., Blair E., Mason T.,
Tetelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M.,
Venter C., Moxon E.R., Grandi G. and Rappuoli R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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ORIGIN
Query Match 94.6%; Score 896.8; DB 1; Length 948;
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Matches 916; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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RESULT 12
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LOCUS AF226521
DEFINITION *Neisseria meningitidis* strain Bz147 gna1220 gene, complete
sequence, and membrane protein GNA1220 (gna1220) gene, complete
cds.
AF226521
VERSION AF226521.1 GI:7228970
KEYWORDS
SOURCE *Neisseria meningitidis*
ORGANISM *Neisseria meningitidis*
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; *Neisseria*.
REFERENCE
AUTHORS Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,

Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storm, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

JOURNAL MEDLINE
20175756
2 (bases 1 to 948)

REFERENCE
Pizza, M., Masiugnani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
Direct Submision
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

JOURNAL
Location/Qualifiers

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ORIGIN

Query Match 94.4%; Score 895.2; DB 1; Length 948;
Best Local Similarity 96.5%; Pred. No. 1.5e-201;
Matches 915; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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RESULT 13
AF226523 948 bp DNA linear BCT 11-MAR-2000
LOCUS
DEFINITION
Neisseria meningitidis strain B2198 membrane protein GNA1220 (gna1220) gene, complete cds.
ACCESSION
AF226523
VERSION
AF226523.1 GI:7228874
KEYWORDS
Neisseria meningitidis
SOURCE
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 948)
Pizza, M., Scariato, V., Masiugnani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Luzzi, B., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storm, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.
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JOURNAL MEDLINE
20175756
2 (bases 1 to 948)

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Location/Qualifiers

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Dd	121	ACGCGCGGTTGGAATTTTGAATTTTGAATTTCCCTTATCCAGACCGGTGCGCTAACCGCATTCGCTG
Oy	181	AAAAGAAATCCCTTTAGAGGTACCAGCCAGCGAGTCTCATCACGCGCATTAATACGAAATTG
Dd	181	AAAAGAAATCCCTTTAGAGGTACCAGCCAGCGAGTCTCATCACGCGCATTAATACGAAATTG
Oy	241	ACTGTGACGCGCATCATCTTAATTTCCAGTAACCGAATCCCAACTCGCTCATACGAGTTG
Dd	241	ACAGTTGACGCGCATCATCTTAATTTCCAGTAACCGAATCCCAACTCGCTCATACGAGTTG
Oy	301	AGCAACTACATTAATGSCAATTTCCACAGCTTGCCCAACGACGCTGCTTCGTTATCGGG
Dd	301	AGCAACTACATTAATGSCAATTTCCACAGCTTGCCCAACGACGCTGCTTCGTTATCGGG
Oy	361	CGTATGAGTTGGAAGAAAAAGTTTGAAGAACCGCAAGAAATCAACAGTACGTCGTCTGC
Dd	361	CGTATGAGTTGGAAGAAAAAGTTTGAAGAACCGCAAGAAATCAACAGTACGTCGTCTGC
Oy	421	GCCCTCGATGAAGCGCGCGGAGCTTGGGGTGTGAAGAGTTCTCCGTTACGAATCAAGAGAT
Dd	421	GCCCTCGATGAAGCGCGCGGAGCTTGGGGTGTGAAGAGTTCTCCGTTACGAATCAAGAGAT
Oy	481	TTCGTTCCGCGCGCAAGAAATCTTTCGCGGAATGACGACCAATTTACCGCGCAAGCGGAA
Dd	481	TTCGTTCCGCGCGCAAGAAATCTTTCGCGGAATGACGACCAATTTACCGCGCAAGCGGAA
Oy	541	AAAGCGCGCCGTAATGCGGAATCCGGAAGCGCGTAAATGGAACAAATCAACCTTGCGAGT
Dd	541	AAAGCGCGCCGTAATGCGGAATCCGGAAGCGCGTAAATGGAACAAATCAACCTTGCGAGT
Oy	601	GCTCAGCGTGAAGCGCAAAATCCCAACATTCGAAGGCGAGGCTCAAGCTTCGAGTCAATGCG
Dd	601	GCTCAGCGGGAAGCGCAAAATCCCAACATTCGAAGGCGAGGCTCAAGCTTCGAGTCAATGCG
Oy	661	TCCAATGCGCAAGAAATCGCCCGCATCAACCGCGCCAAAGGGAAGCGGAATTCCTGCGCG
Dd	661	TCCAATGCGCAAGAAATCGCCCGCATCAACCGCGCCAAAGGGAAGCGGAATTCCTGCGCG

OY		721	CTTGTGTCGGAAGCAATGCAGGACCATCCGGCAATTGCCGCGCCTTGAAACCAA	780
Dd		721	CTTGTGTCGGAAGCAATGCAGGACCATCCGTAATTGCCGCGCCTTGAAACCAA	780
OY		781	GCGGCGGCGGATCGGTGCATCTGAAGATTGCGGAACAATACGTAGCCGGTTCAACAAT	840
Dd		781	GCGGCGGCGGATCGGTGCATCTGAAGATTGCGGAACAATACGTAGCCGGTTCAACAAT	840
OY		841	CTTGCCCAAGAAGCAATAGCGTGATTATGCCCCCAATTGTSCCGACATCGGAGCCTG	900
Dd		841	CTTGCCCAAGAAGCAATAGCGTGATTATGCCCCCAATTGTSCCGACATCGGAGCCTG	900
OY		901	ATTCTTCGCGGCATGAAAAATTTATCGACAGAGCAAAAACCSCCAATAA	948
Dd		901	ATTCTTCGCGGCATGAAAAATTTATCGACAGAGCAAAAACCSCCAATAA	948
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AF226533				
LOCUS				
DEFINITION				
Neisseria meningitidis strain NG28 membrane protein GNA1220				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
Neisseria meningitidis Neisseria meningitidis Bacteria; Proteobacteria; Betaproteobacteria; Neisserieses; Neisseriaceae; Neisseria. 1 (bases 1 to 948) Pizza,M., Scarlato,V., Masignani,V., Giuliani,M.M., Arico,B., Comanducci,M., Jennings,G.T., Baldi,L., Bertolino,E., Capecci,B., Galeotti,C.L., Iuzzi,B., Mancetti,R., Marchetti,E., Mora,M., Nuti,S., Rattai,G., Santini,L., Savino,S., Scarselli,M., Stormi,E., Zuo,P., Brocker,M., Hundt,E., Knapp,B., Blair,E., Mason,T., Tetteljin,H., Hood,D.W., Jeffries,A.C., Saunders,N.J., Granoff,D.M., Venter,C., Moxon,E.R., Grandi,G. and Rappuoli,R. Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing Science 287 (5459), 1816-1820 (2000)				
REFERENCE				
AUTHORS				
Pizza,M., Masignani,V., Comanducci,M., Tetteljin,H. and Rappuoli,R.				
JOURNAL				
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron SPA, Via Fiorentina, 1, Siena 53100, Italy				
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gene				
ORIGIN				

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Qy	61	GTATATCCCGCAGAGAGTCCAGCTTGTGAAAGGCTCGGCGTTTCATCGCGCTTG	120	
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Qy	241	ACTGTTGACGGCATCATCTTATTTTCAAGTAACCGATCCAACTGCTTCATACGCTTG	300	
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Qy	301	AGCAATCTAATTTTGGCAATTTACCGACCTTGCCCAACGAGCTGGCTTCCCTTATCGG	360	
Db	301	AGCAATCTAATTTTGGCAATTTACCGACCTTGCCCAACGAGCTGGCTTCCCTTATCGG	360	
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Qy	421	GCCCTTGATGAGACCGCGCGGCGCTTGGAAGTCTCCGTTACGAATCAAGAT	480	
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Qy	481	TTGGTTCCCGCGGAGAAATCTTTGCGGCAATGACGACCAATTTACCGCGCAACCGCA	540	
Db	481	TTGGTTCCCGCGGAGAAATCTTTGCGGCAATGACGACCAATTTACCGCGCAACCGCA	540	
Qy	541	AAACGGCGCGCTTATTCGCGCAATCGAAGGCGCTTAAATGCAACAAATCACTTGCAGT	600	
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Db	601	GCTCAGCGTGAAGCCCAATTCACCAATCCGAAGCGCGCTGAGCTGCGCTCAATGCG	660	
Qy	661	TCCATGCGGAGAAATCGCGCGCATCAACCGCGCAAGCGCAAGCGCAATCTTGC	720	
Db	661	TCCATGCGGAGAAATCGCGCGCATCAACCGCGCAAGCGCGCAAGCGCAATCTTGC	720	
Qy	721	CTTGTTCGCGAAGCAATGCGAAGCGCATCGTCAATTTGCGCGCGCTTCAACCCAA	780	
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Qy	901	ATTTCGCGCGATGAAATTTATGACAGAGCAAAACCGCAATTA 948		
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RESULT 15
AF226512 948 bp DNA linear BCT 11-MAR-2000
LOCUS AF226512
DEFINITION Neisseria meningitidis strain 205900 membrane protein GNA1220

ACCESSION	AF226512	gene, complete cds.
VERSION	AF226512.1	GI:7228853
KEYWORDS		
SOURCE	Neisseria meningitidis	
ORGANISM	Neisseria meningitidis	
REFERENCE	1 (bases 1 to 948)	
AUTHORS	Pizza, M., Scarlato, V., Maignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capocchi, B., Galeotti, C.L., Iuzzo, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Sanders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.	
TITLE	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing	
JOURNAL	Science 287 (5459), 1816-1820 (2000)	
MEDLINE	20175756	
PubMed	10710308	
REFERENCE	2 (bases 1 to 948)	
AUTHORS	Pizza, M., Maignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.	
JOURNAL	Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy	
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Best Local Similarity	96.2%;	Pred. No. 2.1e-200;
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		Gaps 0;
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LOCUS Neisseria meningitidis strain E32 membrane protein GNA1220
DEFINITION (GNA1220) gene, complete cds.
ACCESSION AF226527
VERSION AF226527.1 GI:7228882
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 948)
Piazza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B.,
Galeotti, C.L., Luzzati, E., Manetti, R., Marchetti, E., Mora, M.,
Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E.,
Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
Tetzelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
Venier, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
JOURNAL
MEDLINE
PUBMED
20175756
10710308

REFERENCE 2 (bases 1 to 948)
AUTHORS Piazza, M., Masignani, V., Comanducci, M., Tetzelin, H. and Rappuoli, R.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
Stena, Chiron SpA, Via Fiorentina, 1, Stena 53100, Italy
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ORIGIN
Query Match 93.9%; Score 890.4; DB 1; Length 948;
Best Local Similarity 96.2%; Pred. No. 2.1e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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RESULT 17 948 bp DNA linear BCT 11-MAR-2000
AF226541
LOCUS Neisseria meningitidis strain Z2491 membrane protein GNA1220
DEFINITION (gna1220) gene, complete cds.
ACCESSION AF226541 GI:7228910
VERSION AF226541
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Pizzia M., Scariato V., Masiqani V., Giuliani M.M., Arico B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon B.R., Grandi G. and Rappuoli R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCES
AUTHORS
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JOURNAL
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ORIGIN
Query Match 93.9%; Score 890.4; DB 1; Length 948;
Best Local Similarity 96.2%; Pred. No. 2.1e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Qy 481 TTGGTTCCCGCGCAAGAAATCCTTCGCGCAATGCAAGCAATTAACCGCGAAGCGAA 540
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Qy 541 AAAACGCGCGGTATTCGCCGAATCCGAAGCGCTGAATGAACAAATCAACTTGCAGT 600
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Qy 601 GGTCAAGCTGAAAGCCGAATTCACAATCCGAAAGCGAGCTCAGGCTGCGCAATGCG 660
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Db 661 TCCAAATGCCGAATAATCCCGGCATCAACCGCGCCAAAGGCGAAGCGGAATCCCGCGC 720
Qy 721 CTGTGTGCGGAAGCCATGCGCGAAGCCATCCGTCAATTCGCCCGCCCTTCAACCCAA 780
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Qy 781 GCGCGGCGCGATGCGGTCATCTGAAGATTGCGGAAACAATAGCTAGCCGCTTCAACAT 840
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Qy 841 CTTCGCAAGAAAGCAATGCGCTGATTATGCGCGCAATGTTGCCGACATCGGACGCTG 900
Db 841 CTTCGCAAGAAAGCAATGCGCTGATTATGCGCGCAATGTTGCCGACATCGGACGCTG 900

QY 901 ATTTGCGCGGATGAAAAATTATCGACAGCAGCAAAAACCGCCAAATTA 948
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RESULT 18
AX043933
LOCUS Sequence 12 from Patent WO0066791. 948 bp DNA linear PAT 24-NOV-2000
DEFINITION AX043933
ACCESSION AX043933 GI:11342856
VERSION
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE
AUTHORS
1 Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.,
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 12 09-NOV-2000;
JOURNAL CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES
location/Qualifiers
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/organism="Neisseria meningitidis"
/mol_type="unassigned DNA"
/db_xref="taxon:487"

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Query Match 93.9%; Score 890.4; DB 6; Length 948;
Best Local Similarity 96.2%; Pred. No. 2.1e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCATTAATCTTGTGGAGCGCGCTTGGCTTCAATCTTTGTC 60
Db 1 ATGGAATTTTCATTAATCTTGTGGAGCGCGCTTGGCTTCAATCTTTGTT 60

QY 61 GTGATCCCCCAGCAGAAATCCACGTTGTCGAAAGGCTGGGCGTTTCATGCGCCCTG 120
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QY 121 AGGCGCGGTTGAATTTTGAATTCCTTATCGACGCGGTGCGCTACCGCCATTGCGTG 180
Db 121 AGGCGCGGTTGAATTTTGAATTCCTTATCGACGCGGTGCGCTACCGCCATTGCGTG 180

QY 181 AAAGAATCCCTTGAACGTACCCAGCCAGCTCTGCATCAGCGCGATTAATCGCAATTG 240
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Db 481 TTGGTTCCGCGGAGAAATCTCTGCGATGCAATGCAAGGCGCAATTCCTGTAAGCGGA 540

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Db 601 GGTGAGCGTGAAGCGGAATTCACATCCGAAGGCGAGGCTGAGGCTGCGTCAATGCG 660

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QY 781 GCGCGGCGGATGCGGCTCAATCTGAAAGATTGCGGAACATACGTGCGCGCTTCAACAT 840
Db 781 GCGCGTGGGATGCGGCTCAATCTGAAAGATTGCGGAACATACGTGCGCGCTTCAACAT 840

QY 841 CTTGCCAAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCCGACATGCGCAGCTG 900
Db 841 CTTGCCAAAGAAAGCAATACGCTGATTAATGCGCGCAATGTTGCCGACATGCGCAGCTG 900

QY 901 ATTTCTGCGCGCATGAAATTAATTCAGACAGCAGCAAAAACCGCCAAATTA 948
Db 901 ATTTCTGCGGATGAAAAATTATCGACAGCAGCAAAAACCGCCAAATTA 948

RESULT 19
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LOCUS Sequence 18 from Patent WO0066791. 948 bp DNA linear PAT 24-NOV-2000
DEFINITION AX043939
ACCESSION AX043939 GI:11342859
VERSION
KEYWORDS
SOURCE
ORGANISM
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE
AUTHORS
1 Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,
Scarlato, V., Rappuoli, R., Frazer, C.M. and Grandi, G.,
Neisseria genomic sequences and methods of their use
Patent: WO 0066791-A 18 09-NOV-2000;
JOURNAL CHIRON CORPORATION (US) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)
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location/Qualifiers
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/organism="Neisseria meningitidis"
/mol_type="unassigned DNA"
/db_xref="taxon:487"

ORIGIN
Query Match 93.9%; Score 890.4; DB 6; Length 948;
Best Local Similarity 96.2%; Pred. No. 2.1e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCATTAATCTTGTGGAGCGCGCTTGGCTTCAATCTTTGTC 60
Db 1 ATGGAATTTTCATTAATCTTGTGGAGCGCGCTTGGCTTCAATCTTTGTT 60

QY 61 GTGATCCCCCAGCAGAAAGTCCACGTTGTCGAAAGGCTGGGCGTTTCATGCGCCCTG 120
Db 61 GTGATCCCCCAGCAGAAAGTCCACGTTGTCGAAAGGCTGGGCGTTTCATGCGCCCTG 120

QY 121 AGGCGCGGTTGAATTTTGAATTCCTTATCGACGCGGTGCGCTACCGCCATTGCGTG 180
Db 121 AGGCGCGGTTGAATTTTGAATTCCTTATCGACGCGGTGCGCTACCGCCATTGCGTG 180

QY 181 AAAGAATCCCTTGAACGTACCCAGCCAGCTCTGCATCAGCGCGATTAATCGCAATTG 240
Db 181 AAAGAATCCCTTGAACGTACCCAGCCAGCTCTGCATCAGCGCGCAATACGAGCTG 240

QY 241 ACTGTTGAGCGCATCTCTATTTCAGTAACCGATCCCAATCGCTTCATACGGTTTG 300
Db 241 ACTGTTGAGCGCATCTCTATTTCAGTAACCGATCCCAATCGCTTCATACGGTTTG 300

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Db      301 |AGCAACTACATTAATGGCAATTACCCAGCTTCCCAACGACGCTGCTTCGTTATCGGG 360
Qy      361 |CGTATGAGTTGACCAAAAGCTTTGAAGAACGCGACCAAAATCAACAGTACCCTGCTCC 420
Db      361 |CGTATGAGTTGACCAAAAGCTTTGAAGAACGCGACCAAAATCAACAGTACCCTGCTCC 420
Qy      421 |GCCCTGATGAAGCCGCGGGGCTTGGGGTGTGAAGATCTCCGCTTACGAATCAAGAT 480
Db      421 |GCCCTGATGAAGCCGCGGGGCTTGGGGTGTGAAGATCTCCGCTTACGAATTAAGAC 480
Qy      481 |TTGGTTCCGCGCGCAAGAAATCTTTGCGCAATGCGGCAAAATTAACCGCGAA 540
Db      481 |TTGGTTCCGCGCGCAAGAAATCTTTGCGCAATGCGGCAAAATTAACCGCGAA 540
Qy      541 |AAACGCGCCGCTATTCGCGAATCCGAAGCGCGTAAATCGAACAAATCAACTTGCAGT 600
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Qy      601 |GGTCAAGCGTGAAGCCGAAATCCCAACATCCGAAGCGGCTCAAGCTGCGGTCATGCG 660
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Qy      661 |TCCATCCCGCAAGAAATCGCCCGCATCAACCGCGCAAGCGCAATCCCTGCGC 720
Db      661 |TCAATTCGCGAAGAAATCGCCCGCATCAACCGCGCAAGCGCAATCCCTGCGC 720
Qy      721 |CTTGTTCGCGAAGCAATGCGCAATCCGATCCGTTCAATTTGCCCGCTTCAAAACCA 780
Db      721 |CTTGTTCGCGAAGCAATGCGCAATCCGATCCGTTCAATTTGCCCGCTTCAAAACCA 780
Qy      781 |GGGCGGCGGATGCGGTCATCTGAAGATTCGCGAACAATPACGTCGCGGTTCAACAT 840
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Qy      841 |CTTGCCCAAGAAAGCAATACGCTGATTAATGCGCCCAATGTTGCCGATCGCGAGCTG 900
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Qy      901 |ATTTCTGCGCGCATGAAAATTATGACAGCAGCAAAACCGCAATTA 948
Db      901 |ATTTCTGCGCGCATGAAAATTATGACAGCAGCAAAACCGCAATTA 948

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RESULT 20
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LOCUS      Nisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION segment 4/7.
VERSION    AL162755 AL157959
KEYWORDS   AL162755.2 GI:7379742
SOURCE     Nisseria meningitidis Z2491
ORGANISM   Nisseria meningitidis Z2491
            Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
            Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 331801)
AUTHORS   Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
            Klee,S.R., Morelli,G., Baeham,D., Brown,D., Chillingworth,T.,
            Davies,R.M., Davis,P., Devlin,K., Felwell,T., Hamlin,N.,
            Holtroff,S., Jagsels,K., Leather,S., Moule,S., Mungall,K.,
            Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
            Skellon,V., Whitehead,S., Spratt,B.G. and Barrall,B.G.
TITLE     Complete DNA sequence of a serogroup A strain of Neisseria
            meningitidis Z2491
JOURNAL   Nature 404 (6777), 502-506 (2000)
MEDLINE   20222556
PUBMED   10761919
REFERENCE 2 (bases 1 to 331801)

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AUTHORS   Parkhill,J.
TITLE     Direct Submission
JOURNAL   Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
            sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
            Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT   Notes:
            Details of N. meningitidis sequencing at the Sanger Centre are
            available on the World Wide Web.
            (URL, http://www.sanger.ac.uk/Projects/N\_meningitidis/).
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/pseudo

117..1333

/gene="NMA1040"

/note="NMA1040, possible type I restriction-modification system specificity protein, pseudogene, len: 1217 bp; N-terminus shows weak similarity to the C-terminal half of TR:O50359 (EMBL:125415), hds1B, Mycoplasma pulmonis restriction-modification enzyme subunit S1B (336 aa), fasta scores; E(): 2.3e-06, 26.2% identity in 141 aa overlap and to many hypothetical restriction-modification subunits. Also similar to NMA1041, fasta scores; E(): 4.8e-10, 37.0% identity in 100 aa overlap. C-terminal similar to part of SW:Y151 ECOLI (EMBL:X13145), hds, Escherichia coli type I restriction enzyme EcoRI2411, specificity protein (410 aa), fasta scores; E(): 1.9e-14, 39.6% identity in 182 aa overlap. Similar to NMA1040, E(): 2.9e-09, 38.0% identity in 100 aa overlap. Contains Pfam match to entry PF01420 Methylase_S, Type I restriction modification DNA specificity domain. Contains a G(8) tract which would allow translation as an intact CDS, if variable. Lies within a region of unusually low GC content"

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/transl_table=11

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/complement(157..166)

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CDS

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misc_feature

repeat_region

misc_feature

misc_feature

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291 aa; similar to parts of many e.g. SW:TIPI_ECOLI
(EMBL:X13145), hsdR, Escherichia coli type I restriction
enzyme Ecor124II R protein (EC 3.1.21.3) (103 aa), fasta
scores; E(): 0, 73.9% identity in 291 aa overlap (frame
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127 aa overlap (frame 1), followed by a frameshift near a
poly-A tract, E(): 0, 72.5% identity in 604 aa overlap
(frame 3)"
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/note="NMA1045, c1pA, probable ATP-dependent protease
ATP-binding protein, len: 759 aa; similar to many e.g.
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ATP-dependent c1p protease ATP-binding subunit (758 aa),
fasta scores; E(): 0, 56.2% identity in 762 aa overlap.
Similar to NMA1683, fasta scores; E(): 0, 37.2% identity
in 844 aa overlap. Contains Pfam match to entry PF00495
c1pA/B, Chaperonin c1pA/B, PS00871 Chaperonins c1pA/B
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DIALSRFQKIDIVEPTVSETVOILKGLPMFEGFHQVATIGALBAALASRTINE
RELPDVAIDVMDAGAAQRIKPSKQKVIQKAQLETVIAKAAIPEKTVSHDDQVL
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yljA, Escherichia coli hypothetical protein (103 aa),
Query Match 93.9%; Score 890.4; DB 1; Length 331801;
Best Local Similarity 96.2%; Pred. No. 2,5e-200;
Matches 912; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1 ATGGAATTTTCATTATCTTGTGGACGCGTTCGCTTTCGCTTCAATCCTTTGTC 60
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RESULT 21
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 LOCUS AX043931
 DEFINITION Sequence 10 from Patent WO0066791.
 ACCESSION AX043931
 VERSION AX043931.1 GI:11342855
 KEYWORDS
 SOURCE Neisseria gonorrhoeae
 ORGANISM Neisseria gonorrhoeae
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE
 1 Piazza, M., Hickey, E., Peterson, J., Tettelin, H., Venier, J.C., Masidrani, V., Galeotti, C., Mora, M., Ratti, G., Scarcellini, M., Scarlati, V., Rappunli, R., Frazer, C.M., and Grandi, G.
 Neisseria genomic sequences and methods of their use
 Patent: WO 006791-A 10 09-NOV-2000;
 CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)

FEATURES
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ORIGIN
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 Qy 61 GTCATCCCGCAGCAGAGTCAAGTTCGAAAGGCTCGGCGCTTTCATCGGCGCTG 120
 Db 61 GTCATCCCGCAGCAGAGTCAAGTTCGAAAGGCTCGGCGCTTTCATCGGCGCTG 120
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 Qy 181 AAAGAATCCCTTGAAGATGACGAGCGAGTTCGATCAAGCGCGATTAATACGAATTG 240
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 Db 841 CTGCGCAAGAAAGCAATACGCTGATTATGCGCGCAATGTCGCAATCGGAGCTG 900
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 Db 901 A-TTTCGCGCGCATGAAATTTATCGACAGAGCAAAACCGCCAA 947

RESULT 22
 AF226517 948 bp DNA linear BCT 11-MAR-2000
 LOCUS AF226517
 DEFINITION Neisseria meningitidis strain 90/18311 membrane protein GNA1220 (gna1220) gene, complete cds.
 ACCESSION AF226517
 VERSION AF226517.1 GI:7228863
 KEYWORDS
 SOURCE Neisseria meningitidis
 ORGANISM Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE
 1 (bases 1 to 948)
 Piazza, M., Scarlati, V., Masidrani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capecechi, B., Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarcellini, M., Storni, E., Zuo, P., Broeker, M., Hunte, E., Knapp, B., Blat, E., Mason, T., Tettelin, H., Hood, E.R., Grandi, G., and Rappunli, R.
 Venier, C., Moxon, E.R., Grandi, G., and Rappunli, R.
 Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 20175756

FEATURES	source
PUBMED 10710308	
REFERENCE 2 (bases 1 to 948)	
AUTHORS Piza, M., Maignani, V., Comanducci, M., Tetteijn, H. and Rappuoli, R.	
TITLE Direct Submission	
JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy	
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ORIGIN	
Query Match 93.2%; Score 884; DB 1; Length 948;	
Best Local Similarity 95.8%; Pred. No. 6.8e-199;	
Matches 908; Conservative 0; Mismatches 40; Indels 0; Gaps 0;	
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Db	601	GGTCAAGGCGGAAGCCGAATTCACCAATTCGGAAGCGAAGGCTCAGAGCTGGGTCAATGCG	660
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Db	661	TCGAATGCCGAGAAATATCGCCCGCATCAACCGCGCCCAAGGTAAGGGAATCTTGGCG	720
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Db	721	CTTGTTGCCGAGCAATGCGGAAGCCATCGTCAAAATTTGCGCGCCCTTTCAAAACCA	780
OY	781	GGCGGGGCGCATGGGTTCATCTGAAGATTGCCGACACAAATACGTAAGCGGCTTCAACAAT	840
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OY	841	CTTGCGCAAAAGAACCAATACGCTGATTAATGCGCCGCAATGTTGCCGACATCGGAGCGTG	900
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OY	901	ATTTCGCGCGCATGAAATATTATGACAGCAGCAAAACCGCCAAATTA	948
Db	901	ATTTCGCGCGGTATGAAATATTATGACAGCAGCAAAACCGCCAAATTA	948
RESULT 23			
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LOCUS		Neisseria meningitidis strain 93/4286 membrane protein GNA1220	
DEFINITION		(gna1220) gene, complete cds.	
ACCESSION		AF226518	
VERSION		AF226518.1 GI:7228865	
KEYWORDS			
SOURCE			
ORGANISM		Neisseria meningitidis	
		Neisseria meningitidis	
		Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
		Neisseriaceae; Neisseria.	
REFERENCE		1 (bases 1 to 948)	
AUTHORS		Pizza, M., Scariato, V., Masiugani, V., Giuliani, M.M., Arico, B.,	
		Comanducci, M., Jemings, G.T., Baldi, L., Bartolini, E., Capechi, B.,	
		Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, E., Mora, M.,	
		Muti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E.,	
		Zuo, P., Broecker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,	
		Tetzelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Grandoff, D.M.,	
		Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.	
		Identification of vaccine candidates against serogroup B	
		meningococcus by whole-genome sequencing	
		Science 287 (5459), 1816-1820 (2000)	
JOURNAL			
MEDLINE		201705756	
PUBMED		10710308	
REFERENCE		2 (bases 1 to 948)	
AUTHORS		Pizza, M., Masiugani, V., Comanducci, M., Tetzelin, H. and Rappuoli, R.	
JOURNAL		Direct Submission	
		Submitted (15-JAN-2000) IRIS Immunobiological Research Institute in	
		Stena, Chiron Spa, Via Fiorentina, 1, Stena 53100, Italy	
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gene			
CDS			

ORIGIN

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Query Match 93.2%; Score 884; DB 1; Length 948;
 Best Local Similarity 95.8%; Pred. No. 6.8e-199;
 Matches 908; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db 841 CTGTCGAAGAAAGCAATAGCGTGAATGCGCGCAATGTTGCGGCAATCGGAGCTG 900

Qy 901 ATTTGCGCGGATGAAATTAATGACAGCAGCAAAACCGCAATTA 948

Db 901 ATTTGCGCGGATGAAATTAATGACAGCAGCAAAACCGCAATTA 948

RESULT 24
 AF226539

LOCUS
 DEFINITION
 Neisseria meningitidis strain NG165 membrane protein GNA1220
 (gna1220) gene, complete cds.
 AF226539
 AF226539.1 GI:7228906

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 1 (bases 1 to 948)
 Pizza, M., Scarlato, V., Masiugnani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Jennings, G.T., Baldi, L., Barcolini, E., Capocchi, B.,
 Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M.,
 Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,
 Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,
 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 2 (bases 1 to 948)
 Pizza, M., Masiugnani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
 Direct Submision
 Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

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ORIGIN

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 Best Local Similarity 95.8%; Pred. No. 6.8e-199;
 Matches 908; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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 1 ATGGAATTTTCTATCTTTGTTGGACGCGTGGCTTTGGCTTCAATCTTTGTC 60
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D	b	181	AAAGAAATCCCTTTAGACGTACCCAGCCAGCTCTGCAATACCGCGCATTAATACGAAT	240
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D	b	241	ACTGTGACGCGCATCATCTATTTCAGATGACCGATCCCAACTGCGCTCATACGGTTG	300
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Q	y	361	CGTATGAGATTGACAAACGTTTGAGAAACGCGACGAATGCAACAGTACCGTCTCTC	420
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Q	y	901	ATTTCGCGCGCATGAATAATTAATGACAGCAGCAAAACCGCCAAATTA	948
D	b	901	ATTTCGCGCGCATGAATAATTAATGACAGCAGCAAAACCGCCAAATTA	948

RESULT 25
AF226519 948 bp DNA linear BCT 11-MAR-2000
LOCUS AF226519
DEFINITION Neisseria meningitidis strain A22 membrane protein GNA1220
(gna1220) gene, complete cds.
ACCESSION AF226519 GI:7228867
VERSION AF226519.1
KEYWORDS Neisseria meningitidis
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 948)
Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,

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Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B., Galeotti, C.L., Iuzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Rati, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broecker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Sanders, N.J., Granoff, D.M., Venter, C., Woxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)
JOURNAL
MEDLINE
20175756
PUBMED
10710308
2 (bases 1 to 948)
REFERENCE
1
AUTHORS
Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.
JOURNAL
Direct Submission
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy
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Best Local Similarity 95.6%; Pred. No. 3.9e-198;
Matches 906; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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RESULT 26
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 (gna1220) gene, complete cds.
 AF226514
 VERSION AF226514
 KEYWORDS
 SOURCE
 ORGANISM
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE
 AUTHORS
 1 (bases 1 to 948)
 Piazza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
 Galeotti, C.L., Luzzi, E., Manetti, R., Bartolini, E., Cappelletti, B.,
 Ntuli, S., Ratti, G., Santini, L., Savino, S., Scarbelli, M., Storni, E.,
 Zuo, P., Brooker, M., Hunds, B., Knapp, B., Blair, E., Mason, T.,
 Tettelein, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, B.R., Grandi, G. and Rappuoli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

FEATURES
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Query Match 92.7%; Score 879.2; DB 1; Length 948;
 Best Local Similarity 95.5%; Pred. No. 9,4e-198;
 Matches 905; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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ACCESSION	AF226516		
VERSION	AF226516.1		
KEYWORDS	GI:7228661		
SOURCE	Neisseria meningitidis		
ORGANISM	Neisseria meningitidis		
REFERENCE	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
AUTHORS	1 (bases 1 to 948)		
	Piazza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,		
	Comanducci, M., Jennings, G.T., Baldi, L., Barolini, E., Capecci, B.,		
	Galotchi, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M.,		
	Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E.,		
	Zuo, P., Brooker, M., Hundt, E., Knapp, B., Blair, E., Mason, T.,		
	Tetzelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,		
	Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.		
	Identification of vaccine candidates against serogroup B		
	meningococcus by whole-genome sequencing		
	Science 287 (5459), 1816-1820 (2000)		
TITLE	2 (bases 1 to 948)		
JOURNAL	Piazza, M., Masignani, V., Comanducci, M., Tetzelin, H. and Rappuoli, R.		
MEDLINE	Direct Submission		
PUBMED	Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in		
REFERENCE	Siena, Chiron SpA, Via Fiorentina, 1, Siena 53100, Italy		
AUTHORS	Location/Qualifiers		
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PUBMED	/strain="860800"		
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Best Local Similarity	95.5%;	Pred. No. 9.4e-198;		
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QY	901	ATTTCGCGCGATGAAATTTATCGACAGCAAGAAACGCCCAATTA	948	
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DEFINITION	Neisseria meningitidis strain Bz169 membrane protein GNA1220			

(gna1220) gene, complete cds.
AF226522 GI:7228872
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 948)
Piazza, M., Scariato, V., Maignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B., Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tetteilin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
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JOURNAL
MEDLINE
PUBMED
10710308
REFERENCES
2 (bases 1 to 948)
Piazza, M., Maignani, V., Comanducci, M., Tetteilin, H. and Rappuoli, R.
Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron SPA, Via Fiorentina, 1, Siena 53100, Italy
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Query Match 92.6%; Score 877.6; DB 1; Length 948;
Best Local Similarity 95.4%; Pred. No. 2.3e-197;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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RESULT 29
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LOCUS
DEFINITION
Neisseria meningitidis strain B283 membrane protein GNA1220
ACCESSION
AF226525
VERSION
AF226525.1 GI:7228878
KEYWORDS
ORGANISM
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS
1 (bases 1 to 948)
Piazza, M., Scariato, V., Maignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecechi, B., Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tetteilin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing
Science 287 (5459), 1816-1820 (2000)
JOURNAL
MEDLINE
PUBMED
10710308

REFERENCE 2 (bases 1 to 948)
 AUTHORS Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappunli, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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ORIGIN

Query Match 92.6%; Score 877.6; DB 1; Length 948;
 Best Local Similarity 95.4%; Pred. No. 2.3e-197;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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RESULT 30
 AF226529 948 bp DNA linear BCT 11-MAR-2000
 LOCUS
 DEFINITION Neisseria meningitidis strain H44/76 membrane protein GNA1220
 ACCESSION AF226529
 VERSION AF226529.1 GI:7228886
 KEYWORDS
 ORGANISM
 SOURCE
 Neisseria meningitidis
 Neisseria meningitidis
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Neisseria.

REFERENCE 1 (bases 1 to 948)
 AUTHORS Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
 Comanducci, M., Deminige, G.T., Baidi, L., Barcolini, E., Capocchi, B.,
 Galeotti, C.L., Iuzzati, E., Manetti, R., Marchetti, E., Mora, M.,
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 Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
 Venter, C., Moxon, E.R., Grandi, G. and Rappunli, R.
 Identification of vaccine candidates against serogroup B
 meningococcus by whole-genome sequencing
 Science 287 (5459), 1816-1820 (2000)

JOURNAL MEDLINE 10710308
 PUBMED 20175756

REFERENCE 2 (bases 1 to 948)
 AUTHORS Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappunli, R.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in
 Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy
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ORIGIN

Query Match 92.6%; Score 877.6; DB 1; Length 948;
 Best Local Similarity 95.4%; Pred. No. 2.3e-197;
 Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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RESULT 31

AP226530

LOCUS

AP226530 948 bp DNA linear BCT 11-MAR-2000

DEFINITION

(gna1220) gene, complete cds.

ACCESSION

AP226530

VERSION

AP226530.1 GI:7228888

KEYWORDS

Neisseria meningitidis

SOURCE

Neisseria meningitidis

ORGANISM

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 948)

AUTHORS

Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Barcolini, E., Capocchi, B., Galeotti, C.L., Luzzi, E., Manetti, R., Marchetti, B., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Stormi, E., Zuo, P., Brocker, M., Hundt, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M., Venter, C., Woxon, E.R., Grandi, G. and Rappuoli, R.

TITLE

Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing

JOURNAL

Science 287 (5459), 1816-1820 (2000)

MEDLINE

20175756

PUBMED

10710308

REFERENCE

2 (bases 1 to 948)

AUTHORS

Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.

TITLE

Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy

JOURNAL

location/Qualifiers

FEATURES

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ORIGIN

Query Match

92.6%; Score 877.6; DB 1; Length 948;

Best Local Similarity

95.4%; Pred. No. 2.3e-197;

Matches

904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCTATTCCTTTGTGGAGCCGTCGCGTTTCGGCTTCAATCCTTTGTC 60
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LOCUS	AF226540	Neisseria meningitidis strain SWZ107 membrane protein GNA1220	
DEFINITION	(gna1220) gene, complete cds.		
ACCESSION	AF226540.1	GI:7228908	
VERSION	AF226540.1	GI:7228908	
KEYWORDS	Neisseria meningitidis		
SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
REFERENCE	1 (bases 1 to 948)		
AUTHORS	Pizza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B., Comanducci, M., Jennings, G.T., Baldi, L., Bartolini, E., Capecci, B., Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, E., Mora, M., Nuti, S., Ratti, G., Santini, L., Savino, S., Scarselli, M., Storni, E., Zuo, P., Broeker, M., Hunte, E., Knapp, B., Blair, E., Mason, T., Tettelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.O., Granoff, D.M., Venter, C., Moxon, E.R., Grandi, G., and Rappuoli, R.		
TITLE	Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing		
JOURNAL	Science 287 (5459), 1816-1820 (2000)		
MEDLINE	20175756		
PUBMED	10710308		
REFERENCE	2 (bases 1 to 948)		
AUTHORS	Pizza, M., Masignani, V., Comanducci, M., Tettelin, H. and Rappuoli, R.		
TITLE	Direct Submision		
JOURNAL	Submitted (19-JAN-2000) IRIS Immunobiological Research Institute in Siena, Chiron Spa, Via Fiorentina, 1, Siena 53100, Italy		
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ORIGIN			
Query Match	92.6%; Score 877.6; DB 1; Length 948;		

Best Local Similarity 95.4%; Pred. No. 2.3e-197; Matches 504; Conservative 0; Mismatches 44; Indels 0; Gaps 0;			
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DEFINITION	Sequence 14 from Patent WO0066791.		
ACCESSION	AX043935		

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VERSION      AX043935.1  GI:11342857
KEYWORDS
SOURCE       Neisseria meningitidis
ORGANISM     Neisseria meningitidis
              Bacteri; Proteobacteria; Betaproteobacteria; Neisseriales;
              Neisseriaceae; Neisseria.
REFERENCE    1
AUTHORS      Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J.C.,
              Masiugnani, V., Galeotti, C., Mora, M., Ratti, G., Scarfelli, M.,
              Scariato, V., Rappunli, R., Frazer, C.M. and Grandi, G.
              Neisseria genomic sequences and methods of their use
              Patent: WO 0066791-A 14 09-NOV-2000;
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FEATURES
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ORIGIN
Query Match      92.6%; Score 877.6; DB 6; Length 948;
Best Local Similarity 95.4%; Pred. No. 2,3e-197;
Matches 904; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGGAATTTTCAATCTTGTGGCAGCGCGCTTTCGGCTTCAATCCGCGCCTG 60
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            Complete genome sequence of Neisseria meningitidis serogroup B
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 Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
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 REFERENCE
 AUTHORS Pizzo, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C.,
 Masignani, V., Galeotti, C., Mora, M., Ratti, G., Scarcellini, M.,
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 TITLE Neisseria genomic sequences and methods of their use
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 CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
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JOURNAL	Maggiarino, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M.,		
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QY	361	CGTATGAGATTGGACAAACGTTTGAAGAACGAGCAAGATCAACAGTACCGTCGCTCC	420
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Db	Accession	Source	Organism	Reference Authors	Title	Journal	Medline	Pubmed	Reference Authors	Journal	Features
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ACCESSION	AF226526										
VERSION	AF226526.1										
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	Pizza, M., Scarlato, V., Maignani, V., Giuliani, M. M., Arico, B.,										
	Comanducci, M., Jennings, G. T., Baldi, L., Bartolini, E., Capecechi, B.,										
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	Tettelein, H., Hood, D. W., Jeffries, A. C., Saunders, N. U., Granoff, D. M.,										
	Venter, C., Moxon, E. R., Grandi, G. and Rappuoli, R.										
	Identification of vaccine candidates against serogroup B										
	meningococcus by whole-genome sequencing										
	Science 287 (5459), 1816-1820 (2000)										
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MEDLINE	10710308										
PUBMED	2 (bases 1 to 948)										

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ACCESSION
AF226535
VERSION
AF226535.1 GI:7228898
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Piazza, M., Scarlato, V., Masignani, V., Giuliani, M.M., Arico, B.,
Comanducci, M., Jennings, G.T., Baldi, L., Bartoloni, E., Capecechi, B.,
Galeotti, C.L., Iuzzi, E., Manetti, R., Marchetti, B., Mora, M.,
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Tetzelin, H., Hood, D.W., Jeffries, A.C., Saunders, N.J., Granoff, D.M.,
Venter, C., Moxon, E.R., Grandi, G. and Rappuoli, R.
Identification of vaccine candidates against serogroup B
meningococcus by whole-genome sequencing
Science 287 (5439), 1816-1820 (2000)
JOURNAL
MEDLINE
10710308
PUBMED
20175756
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2 (bases 1 to 948)
Piazza, M., Masignani, V., Comanducci, M., Tetzelin, H. and Rappuoli, R.
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